.rni

-733-756-1

-09

an

RECEPTOR HEK

0 3 ..

S

4 .. S \vdash

9

Ju.

Ė

셤

õ

d

ò

엄

δ

õ

ద

d

δ

d

ğ

d

Qγ

g

셤

å

g

δ

D

ò

g

ğ

d

ğ

요

ద

ğ

ò

Ω

```
1007
180
                       239
                               240
                                              300
                                                              360
                                                                             420
                                                                                            480
                                                                                                           540
                                                                                                                                         9
                                                                                                                                                       840
                                       287
                                                      347
                                                                                                                          600
                                                                                                                                 647
                                                                                                                                                                                                     900
                                                                                                                                                                                                             947
                                                                                                                                                                                                                    960
                                                                     407
                                                                                     467
                                                                                                   527
                                                                                                                   587
                                                                                                                                                707
                                                                                                                                                                                              887
                                                                                                                                         scetgge (
                                             ggctt
|||||
               gcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgca
                               ctgctgcgcctccacatcgcactccggggagaagccggtccccactctcccccagttcac
                                                                                                                         cgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                           ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt
                                                                                                                                                                                      ctgcaccatacatct
                                             cagaa
                                                                                                                                                                                                             CGGNG
                                                                                                                                        က
                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                    0-0
                                                                                                                                                                                                                                   gttccagcgctacagc
                              gtgtccgc
|||||||||||
GTGTCCGC
                                                                    348
61
       20
               121
                      80
                                      240
                                              241
                                                     288
                                                                                    408
                                                                                                   468
                                                                                                                                 588
                                                                                                                                                648
                              81
                                                             301
                                                                            361
                                                                                                                  28
                                                                                           421
                                                                                                          481
                                                                                                                          541
                                                                                                                                                               08
                                                                                                                                                                              768
                                                                                                                                                                                             28
                                                                                                                                                                                                     841
                                                                                                                                         601
                                                                                                                                                       661
                                                                                                                                                                      21
                                                                                                                                                                                                            888
                                                                                                                                                                                                                   901
                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                          008
                                                                                                                                                                                     81
                                                                                                                                                                                                                           ω
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                     5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 917.8; DB 1;
Pred. No. 2.4e-179;
); Mismatches 2;
                                                                                                                                                                                     Version
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             US/08/240,124
                                          S: IMMUNEX CORPORATION 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 587-0430
TELEX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.8%;
Matches 919; Conservative
                                                                                                                                                                                              CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
140..796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sig_peptide
83..139
                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TITLE OF INVENTION: RENUMBER OF SEQUENCES. 4
                                                                                     WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83..799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hek-L A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CI
                                                        STREET: 51 UNI
CITY: SEATTLE
STATE: WASHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                 USA
                                                                                                                                                                                                                           FILING DATE:
                                                                                                             98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY:
; LOCATION:
US-08-240-124-1
                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
```

ö

9

276



SURFAC

CELL

HE H

BINDS

P. THAT

RESULT 2
US-08-240-1211
; Sequence 1, Application US/08240124
; Patent No. 5516658
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THE

SULT

3

.. .:

d

Q

ద

Š

임

Ö

ద

a

Q

a

Ω

d

Q

Q

ŏ

d

g

Qγ

ğ

d

QΣ

Ω

d

N

```
720
                                                                                                                                                                                                                                                 780
                                                                                                                                                                                                                                                                           840
                                                                                                                                                                                                                                                                                                      900
                                                                                                                                                                600
                                                                                                                                                                                            9
                                                                                                                                                                                                                                   816
                                                                                                                                                                                                                                                              876
                                                                                                                                                                                                                                                                                         936
                           300
                                         396
                                                      360
                                                                   456
                                                                                 420
                                                                                              516
                                                                                                            480
                                                                                                                        576
                                                                                                                                     540
                                                                                                                                                   636
                                                                                                                                                                              969
                                                                                                                                                                                                        756
 240
              336
                                                                                                                                                                                                                                                 aaggga
|||||||
                                                                                                                                                                                                                                                                                                       acgggg
                                                                                                                                                                                                   CCTGGC
                                                                                                                                                                                                                            CCCCTG
                                                                                                                                                                 tcaggt
                                                                                                                                                                             TCAGGT
gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                                          ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt
                                                                                                                                     ctgctgcgcctccacatcgcactccggggagaagccggtccccactctcccccagttcac
                                                                                                                                                                                                                                                                           cctggc
                                                                                                                                                                                                                      cccctg
                                                                                                                                                                                                                                                                                                     catgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaacct
                                                                                                                                                                                          SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                  CELL
                                                                                                                                                                                                                                                                                                                                                                                                                  THE
                                                                                                                                                                                                                                                                                                                                                                                                                  BINDS
                                                                                                                                                                                                                                                                                                                                                                                                          P.
THAT
HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMUNEX CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                US/0845394
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET
                                                                                                                                                                                                                                                                                                                                                                                                   BECKMANN, M. P.
CERRETTI, DOUGLAS P
NVENTION: CYTOKINE I
                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disk
                                                                                                                                                                                                                                                                                                                                 51 UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                           SESULT 3
JS-08-453-943-1
; Sequence 1, Application U;
; Patent No. 5738844
; GENERAL INFORMATION:
; APPLICANT: BECKMANN,
; APPLICANT: CERRETTI,
; TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: RINUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WASHINGTON: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 51
CITY: SEATT
STATE: WASH
COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE
                                                                                361
                                                                                                                                                                            637
                                                                                                                                                                                           601
                                                                                                                                                                                                                     661
                                                                                                                                                                                                                                   757
                                                                                                                                                                                                                                                721
                                                                                                                                                                                                                                                             817
                                                                                                                                                                                                                                                                           781
                                                                                                                                                                                                                                                                                        877
                                                                                                                                                                                                                                                                                                      841
                                                                                                                                                                                                                                                                                                                   937
                                                                                                                                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                                                                                                             997
                           241
                                                                                             457
                                                                                                          421
                                                                                                                       517
                                                                                                                                     481
                                                                                                                                                                541
                                                                                                                                                                                                        697
                                        37
                                                                  397
                                                                                                                                                  577
                                                      301
             277
                                                                                                                                                                                                                                                                                                                                                                   RESULT
US-08-4
```

d

Q

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 1;
.4e-179;
es 2;
                      Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 917.8;
Pred. No. 2.4e
0; Mismatches
                                                                                                                                            APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
                 SOFTWARE: Microsoft Word for Apple, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
GLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                     APPLICATION NUMBER: US 08/240,124 FILING DATE: 09-MAY-1994 APPLICATION NUMBER: US 08/161,132 FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA:
          System 7
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELERAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.7%;
ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                   CDNA to mRNA
Apple Macintos
SYSTEM: Apple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
140..796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sig_peptide
83..139
                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
83..799
                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                 hek-L A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
919; Conser
                                                                                                                                                                                                                                                                                                                                                         TOPULOS...
MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-453-943-1
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 919
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

ö

156

9

120

216

180

276

240

336

300

396

ţ

.rspt

```
Ltd
4.5
Compugen
 version - 2000
GenCore
(c) 1993
      Copyright
```

OM protein - protein search, using sw model	July 13, 2002, 10:44:50; Search time 65.87 Seconds (without alignments) 625.061 Million cell updates/se	US-09-733-756-2 score: 1301 e: 1 MAAAPLLLLLLVPVPLLPLREHLPLAVGIAFFLMTFLAS 238	table: BLOSUM62 Gapop 10.0 , Gapext 0.5
OM protei	Run on:	Title: Perfect score: Sequence:	Scoring table:

562222 hits satisfying chosen parameters: length: 0 length: 2000000000 $^{\rm ot}$ sed number DB DB Minimum Maximum Total

residues

562222 seqs, 172994929

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

brachydanio
frattus norv
gallus gall
ctenophorus
mus musculu
lbrachydanio
rattus norv
ratt ription 090yc5 b 0923g4 r 098tz1 098tz1 098tz1 090zs8 m 093431 k 090zs8 m 090zs1 090zg7 090zg7 090zg7 090zg7 090zg7 090zg7 Desc SUMMARIES Q90YC5 Q923G4 Q98TZ1 Q98TZ1 Q9PTD0 Q9D7K8 Q9PTD1 Q9PTD1 Q9CRL3 Q9CRL3 Q9CRL3 Q90Z31 Q90Z31 Q90Z31 DB Length 219 202 202 88 206 2209 2209 102 42 42 42 333 333 652 Query Match 55.9 32.6 31.2 31.2 31.2 31.2 28.7 26.0 26.0 19.0 113.7 112.8 727 727 727 406 406 373 373 367 373 367 373 178 178 166.5 166.5 Score Result No.

17 143.5 11.0 348 5 044516 18 138.5 10.6 279 5 094474 19 138.5 10.6 334 13 090232 20 124.5 9.6 341 13 090233 21 100 7.7 377 3 074823 22 96 7.4 1199 5 090233 23 92 7.1 855 15 090823 24 88.5 6.8 441 4 09089 25 88.5 6.8 709 4 09089 26 88.5 6.8 844 4 090824 27 87.5 6.7 765 11 09109 28 87.5 6.7 765 11 09109 29 87.5 6.7 765 11 09109 30 86 6.6 442 11 09220 31 88 6.6 442 11 09520 32 <th>O44516 caenorhabdi Q90432 brachydanio Q90233 brachydanio Q90233 brachydanio O74823 schizosacch Q9v9y3 drosophila Q9v9y3 drosophila Q9nrn2 homo sapien Q9lm29 homo sapien Q9lm29 homo sapien Q9lxv1 mus musculu Q9bzh4 homo sapien Q9bzh4 homo sapien Q95560 caenorhabdi Q9y262 mus musculu Q92217 mus musculu Q92217 mus musculu Q95217 caenorhabdi Q9ykq4 human immun Q17657 caenorhabdi Q9ykq4 human immun Q17657 saccharomyc Q961a1 drosophila Q9ykq4 drosophila Q9yov94 drosophila Q9yov94 drosophila Q9ybp6 drosophila Q9ybbc3 homo sapien Q13648 homo sapien</th> <th></th>	O44516 caenorhabdi Q90432 brachydanio Q90233 brachydanio Q90233 brachydanio O74823 schizosacch Q9v9y3 drosophila Q9v9y3 drosophila Q9nrn2 homo sapien Q9lm29 homo sapien Q9lm29 homo sapien Q9lxv1 mus musculu Q9bzh4 homo sapien Q9bzh4 homo sapien Q95560 caenorhabdi Q9y262 mus musculu Q92217 mus musculu Q92217 mus musculu Q95217 caenorhabdi Q9ykq4 human immun Q17657 caenorhabdi Q9ykq4 human immun Q17657 saccharomyc Q961a1 drosophila Q9ykq4 drosophila Q9yov94 drosophila Q9yov94 drosophila Q9ybp6 drosophila Q9ybbc3 homo sapien Q13648 homo sapien	
7 143.5 11.0 348 5 8 138.5 10.6 279 5 1 138 10.6 334 1 1 100 7.7 377 3 2 92 7.1 855 1 8 88.5 6.8 894 4 8 87.5 6.7 765 1 8 7.5 6.7 894 4 8 87.5 6.7 765 1 8 87.5 6.7 894 4 8 87.5 6.7 765 1 8 87.5 6.7 894 4 8 87.5 6.7 894 4 8 87.5 6.7 894 4 8 88.5 6.4 898 3 8 83.5 6.4 457 3 8 83.5 6.4 473 5 8 83.5 6.4 463 3 8 83.5 6.4 463 3 8 82.5 6.3 304 4	044516 090474 090474 090233 074823 074823 074823 09023 091823 091809 091809 091809 091809 091809 091804 017657 016783 098262 098262 098262 098262 098262 098262 098262 0982672 0982619 0998099 0999999	
7 143.5 11.0 34 8 138.5 10.6 27 1 138 10.6 33 1 124.5 9.6 34 2 96 7.7 37 3 92 7.1 85 6 88.5 6.8 89 8 7.5 6.7 76 8 87.5 6.7 81 8 87.5 6.7 70 8 87.5 6.7 70 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	2 1 11 11 2	
7 143.5 11. 8 138.5 10. 1 138 10. 2 138.5 10. 2 96 7. 3 88.5 6. 8 87.5 6. 8 87.5 6. 8 83.5 6.	#UKKKLI8478778844780444666664 47647666666666666666666666666	
7 1443. 1 143. 1 1 100 124. 1 1 1 100 124. 1 1 1 100 124. 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	660666666666666666666666666666666666666	
11112222222222222222222222222222222222	88 88 88 88 89 7	
	HIII COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	

ALIGNMENTS

RESULT 1	Q90YC5 PRELIMINARY; PRT; 219 AA.	1-DE	(TrEMBLrel, 19,	EPHRIN-A3. EPHRIN-A3.	o rerio (Zebrafish) (Zebra danio).	tazoa; Chordata; Craniata; Vertebrata; E	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes: Cyprinidae: Danio.	NCBI_TaxID=7955;	SEQUENCE FROM N.A.	4122	Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;	entification of ephrin-A3 and novel	MHB in embryonic zebrafish by ordered differential display.";		MBL; ABUSI6/8; BABSS89I.I;	SEQUENCE 219 AA; 25146 MW; /I9192/EU3FBEAUI CRC64;	Query Match Best Local Similarity 61.9%; Pred. No. 1.4e-67; Matches 140: Conservative 25; Mismatches 43: Indels 18: Gaps	MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYL	1 MALYALCLFLTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT) — - -	54 IYCPHYNSSQRGIAEQYVLYMVSYRGYRTCDPQLGFKRWECNRPHAPH 104	121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT 180
RES	A D	DT	DI	C E	OS	ပ္ပ	88	XO	RP R	RX	RA	RŢ	RŢ	R.	7 2	Ŏ S	OME	δγ	qq	:	Ś	qa	Οy

ω ;

2

4

Tue

.rspt

56-2

-733-7

- 09

ns

Γ

```
PS01299; EPHRIN;
   PROSITE;
           NON_TER
SEQUENCE
                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                      4
                                                       Best Loc
Matches
                                                                                                                                     26
                                                                                                                                                       125
                                                                                                                                                                        106
                                                                                                                                                                                         184
                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                              Q9PTD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                   g
                                                                                                                                     g
                                                                                                                                                                                                                                                                       В
                                                                                                                     ô
                                                                                                                                                        ô
                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                          2
KFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHGRSCLRLRVYVCCSTASDSDDEPQPT 164
                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                               182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Idae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E.B.;
ng visual
                                                                                                                                                                                                                                                                                                                         CPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSP1KF
                                                                                        UI-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN A3 (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati
                                                                                                                                                                                                                                                                                                                                                           ----GPGGGAEQYVLYMVNLSGYRTCNASQGSKRWECNRQHASHSPIKF
                                                                                                                                                                                                          ligands
                                                                                                                                                                                         A.,
                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Menzel P., Valencia F., God ment P., Dodelet V.C., Pasquale E. Menzel P., Valencia F., God ment P., Dodelet V.C., Pasquale E. Ephrin-A6, a new ligand for EphA receptors in the developing system.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317286; AAK00944.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                        Length 118
                                                                                                                                                              Craniata; Vertebrata; Eute]
: Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                             FF0277F079783A46 CRC64
               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Last sequence update)
, Last annotation updat
                                                                                                                                                                                                                                                                                        ; DB 11;
3e-53;
                                                                                                                                                                                                                                                                                      Score 586; DB Pred. No. 3e-53; Mismatches
                                                                               118
                                                                                                                                                                                                                                                                                                                                                                                                       --KDFEGENPQVPKLEKSISG
                                                                                                                                                                                                                                                                                                                                                                                               QFTMGPNVKINVLEDFEGENPQVPKLEKSISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; (Neognathae;
                                                                                                                                                                                                                                                            13470 MW;
                                                                                                                                                                                                                                                                                      45.0%;
illarity 72.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-OCT-2001 (TrEMBLrel. 1
EPHRIN-A6 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chord
Archosauria; Aves; Neogna
                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                            118 AA;
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                                           CPHYNSS-
                                                                                     0923G4;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                       110;
                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                      Query Match
Best Local
Matches 11
                                                                              092364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                  qq
                                                                                                                δ
                                                                                       AC
DT
DT
                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             O9PTD0
O9PTD0;
O9PTD0;
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2001 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EPHRIN A3 (FRAGMENT).
Ctenophorus ornatus.
Ctenophorus ornatus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system.";
                                                                                                                                                                                            6 LLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPH
                                                                                                                                             KFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVP-TLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                        Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=BRAIN;
Chen P.B., Rodger J., Dunlop S.A., Beazley L.D.;
"Ephrin homologs are expressed in the adult lizard visual
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE=BRAIN;

Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF209777; AAF19444.1; -.

InterPro; IPR001799; Ephrin.

Pfam; PF00812; Ephrin; 1.
                                                                                          Indels
91E2716FF91353F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C56FCD8B13F219E7 CRC64;
                                                      DB 13;
                                                    Score 424.5; DB 13
Pred. No. 3.8e-36;
; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 406; DB 13;
Pred. No. 1.1e-34;
7; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYS 130
                                                                                      28;
 22624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
10636 MW;
                                                    32.6%;
Similarity 45.4%;
84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 31.2%;
Similarity 75.0%;
72; Conservative
202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=95347;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                             170
                                                                                                                                                                                                                                                                                                                                          FTMGP 188
                                                                                                                                                                                                                                                                                                                                                                             GRGGP
                                                                                                                                                                                                                                 YSA --
```

```
3;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAIN=21085660; Pubbmed=11217851;
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Loyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hayashizaki Y.;

"Functional annotation of a full-length mouse cDNA collection.";

R EMBL; AK012195; BAB28092.1;

R EMBL; AK012195; BAB28092.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN
                                                                                                                                                       tomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |::||||
|PVRFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNA - - SQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                      Euteleost; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEK
                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
10 DAYS EMBRYO CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:2610529M21, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675E32971D1C6EBC CRC64;
                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 11;
3.3e-34;
                206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 406; DB Pred. No. 3.3e 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       093431 PRELIMINARY; PRT; 229 AA 093431; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequence upol-DEC-2001 (TrEMBLrel. 19, Last annotation EPHRIN A-L1. Brachydanio rerio (Zebrafish) (Zebra danio)
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.
MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PR01347; EPHRIN.
; PD002533; EPhrin; 1.
E; PS01299; EPHRIN; 1.
CE 206 AA; 22859 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06643; Efna4.
IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.2%;
larity 46.9%;
Conservative
               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ephrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:10664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00812
             Q9CZS8;
Q9CZS8;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
Pfam; PF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
093431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
Q9C2S8
                             AC
DT
DT
                                                                        RL
DR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DT
DT
DE
DE
OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩĪ
```

```
P SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=TONGUE;

X Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Kamiya M., Lee N.H.,

A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J
F
     Euteleostomi;
Ostariophysi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- AHGEIASQEAERYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : |: ||:
-MVEKVEEIEGKMAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYMVSRNGYRTCNA-SQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K., Cooke J.;
segmentation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGE-
                                                                                                                                                                                                                                                                                                                                                                                   Length 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
ADULT MALE TONGUE CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:2310004J15, FULL INSERT SEQUENCE.
                                                                                                          Durbin L., Brennan C.H., Shiomi K., Cooke J.;
"Eph signalling is required for segmentation and different the somites.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ006838; CAA07264.1; -.
InterPro; IPR001799; Ephrin.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                   Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 229 AA; 26115 MW; 8684462F67AF6F5C CRC64;
     Vertebrata; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                 28.7%; Score 373; DB 1
40.0%; Pred. No. 1e-30;
ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -QVPKLEKSI - - SGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKPLHHHGQECLRLKVDVVGPHGSKNKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 84; Conser
                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- NP--
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09D7K8
09D7K8;
                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9D7K8
    pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
```

9

60-

ns

```
DR
DR
DR
DR
FT
FT
SQ
              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                   δ
                                                        pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID
                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                         9
                       Wilming L.,
                                                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                                                                                                         164
             Storch K.-F.,
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ipheral
of Eph
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                 19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG
                                                                                                                                                                                                                                                                                        PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE
                                                                                                                                                                                                                                                                                                     -KITHNPQAHVNPQEK
                                                                                                                                                                                                                                                       Euteleostomi;
                                          Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection."
Nature 409:685-690(2001).
EMBL; AK009144; BAB26102.1; -.
MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e);
                                                                                                                                                                                                   205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 102
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Matsunaga T., Davis J.G., Greene M.I.;
"Cellular and subcellular compartmentalization of adult vestibular system by distinctive and overlapping express receptors and ephrins.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF131912; AAD33515.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                        UNKNOWN_1.
E37E55767459A4EC CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WUE7;

Q1-NOV-1999 (TrEMBLrel. 12, Created)

01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

EPHRIN A-2 (FRAGMENT).

Rattus norvegicus (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 11;
1.6e-27;
ches 23;
                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                                        Score 367; DB 11;
Pred. No. 3.7e-30;
                                                                                                                                                                                                                                                                                                                                                                             -FEGENPOVPKLEKSISGTSPKREHLPLAVGIAFFLATFLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A497302F7FD7364B
                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.0%; Score 338; Dilarity 58.9%; Pred. No. 1.6 Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                         InterPro; IPRULLOCCE,
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS00678; WD_REPEATS_1;
                                                                                                                                                       ;
                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
                                                                                                                                                                                                  28.2%;
38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephrin; 1.
EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
11838
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY
                                                                                                                                                                                                            Local Similarity
Les 85; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS01299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \begin{array}{c} 102 \\ 102 \end{array}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9WUE7
                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q9WUE7
 q
                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                            ò
```

5

.; 8

Indels

Q-GFKR 107

49 YTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTCNAS

ò

```
Brand M.,
                                                                                                                                                                   09PTD1;
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EPHRIN A2 (FRAGMENT).
Ctenophorus ornatus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      axon pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                       system.";
GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PQPHSRMERYILFMVNHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi
Ostariophys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        φ
•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ž
                                                                                                                                                                                                                                                                                                                                                                      Scarborough M.T.C., Rodger J., Dunlop S.A., Beazley L.D.; "Ephrin homologs are expressed in the adult lizard visual Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF209776; AAF19443.1; -. InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin. 1. ProDom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                             WECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brennan C., Holder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commissural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson S.;
"The Pax protein Noi protein is required for commissural formation in the rostral forebrain.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases EMBL; Y12928; CAA73391.1; -.
ZFIN; ZDB-GENE-001128-1; efna5a.
InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BD561F18D34C0F28 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 268.5; DB 1
Pred. No. 2.4e-20;
3; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strable U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93
11323 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.6%;
larity 49.5%;
Conservative 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       042304;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
MacDonald R., Scholes J.,
                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
EPHRIN-AS (FRAGMENT).
EFNASA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
48; Conser
                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=95347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                          SEQUENCE TO TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                               Ctenophorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          042304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
                  П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35
                                               108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
                                                                                                                          RESULT
Q9PTD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
042304
```

2

```
SEQUENCE FROM N.A.
Hirate Y., Mieda M., Harada T., Yamasu K., Okamoto H.;
"A systematic search for the downstream target genes of the midbra:
"A systematic search for the downstream target genes of the midbra:
MHB reciprocal inductive signaling by ordered differential display revealed the expression of ephrin-A3 in the posterior tectum of zebrafish embryos.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055674; BAB62805.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rkeliminary; PRT; 331 AA.
090231;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN B3.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21290827; PubMed=11397014;
Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
"Morphogenesis of prechordal plate and notochord requires intact eph/ephrin b signaling.";
Dev. Biol. 234:470-482(2001).
EMBL; AF375227; AAK64277.1; -.
SEQUENCE 331 AA; 35638 MW; 6A5EACD509A09818 CRC64;
                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, D160 PROTEIN (FRAGMENT).
                                                                                          0902G7;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; ABO
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 33
                                                                             Q90ZG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                       D160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59
                                          RESULT
0902G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
Q90231
                                                                                                                                                                   DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STAIN=C57BL/6J;

C TISSUE-EMBRYONIC BODY BETWEEN DIAPHRAGM REGION, AND NECK;

MEDLINE=21085660; PubMed=11217851,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Mashima J., Mazzarelli J., Mombaerts P.,

RA Asaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Toyo-oka K., Wang K.H., Waitz C., Whittaker C., Wilming L.,

Wurnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                    3
                                                                                                                                                                    Gaps
                                                                                                                                                                                                    -NASQG
                                                                                                                                                                                                                                        DHTAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INSERT
                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA collectio
                                                                                                                                œ
                                                                                                                                                                                               REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGFGGGAEQYVLYMVSRNGYRTC
                                                                                                                                                                                                                     -VPEERTERYVLYMVNYDGYSSC
                                                                                                                                                                                                                                                                                                                                                                                                     U1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
12 DAYS EMBRYO EMBRYONIC BODY BETWEEN DIAPHRAGM REGION AND RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE:9430025D14, FULL EFNA3.
                                                                                                                                Length
                                                                                                                                                                   Indels
                                                                          CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64
                                                                                                                           DB 13;
                                                                                                                          Score 247.5; DB 13
Pred. No. 3.1e-18;
6; Mismatches 17;
                                                                        712DDC6058214993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55DB95E5E0B1B0E2
                                                                                                                                                                                                                                                                                                                                                                                                42
                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                     FKRWECNRPHAPHSPIKFSEKFQRYS
                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                    19.0%;
51.2%;
                      _
                                                                       MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a Nature 409:685-690(2001). EMBL; AK020438; BAB32100.1; MGD; MGI:106644; Efna3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4569 MW;
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin;
                                                                                                                                                              Conservative
                                                     80
9674
                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                         l Similarity
44; Conserv
                                                                       80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                       55
                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                 46
                                                                                                                                                                                                                                  m
                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                           9CRL3
DR
DR
FT
SO
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                 õ
```

ü

5;

Length 70

; DB 13; 4.4e-11; ches 12;

Score 178; DB Pred. No. 4.4e 4; Mismatches

13.7%; larity 54.1%; Conservative 14

Similarity 33; Conser

59

->

14;

91F2BE4E657E10FD CRC64

7621 MW;

70 AA;

CCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLA

midbrain

Euteleostomi;
Ostariophysi

update)

Last sequence update)
Last annotation updat

Created)

70

PRT;

PRELIMINARY;

```
12;
                                                      63
                                                      LLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN
              331;
                                                                  -
-
-
               Length
                                   Indels
             DB 13;
                                  88;
             12.8%; Score 166.5; DB 26.8%; Pred. No. 5e-09; iive 28; Mismatches
                                                                 --
--
--
--
                                  Conservative
     Query Match
Best Local Similarity
...tches 70; Conserva
                                                      ò
                       ö
                       Gaps
                      0;
   42;
                      Indels
   Length
                                          238
                                                              42
                                     Score 208; DB 11;
Pred. No. 1.7e-14;
0; Mismatches 1
16.0%;
illarity 97.6%;
Conservative
```

Similarity

41;

Best Loc Matches

ò

ŏ

Š

ŏ

.rspt

```
13;
                            112
                                                                            172
                                                     104
                                                                                                      157
                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPSV 191
   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      igands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
 -NMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                            -NGYRTCNASQGFKRWECNR
                                                                           PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSH
                                                                                                                              --INVLEDFEGE--NPQVPKLEKSISGTSPKREH
                                                                                                                                           :omi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYWNSSNOHLR-REGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGFGGGAEQYVLYMV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --LLTCDR---PSQDLRFTIKFQEFSPNLWGHEFQSQRDYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SRNGYRTCNASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- MGPNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- AVGIAFFLMTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PNPDIPNVGET-SGNATKTGENGPLPISHVPLVAGAAGGAALLLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20099673; PubMed=10633856;
Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H
Wilkinson D.G., Brandli A.W.;
"Comparative analysis of embryonic gene expression defines pointeraction sites for Xenopus EphB4 receptors with ephrin-B l.Dev. Dyn. 216:361-373(1999).
EMBL; AJ236866; CAB65511.1; -.
InterPro; IPR002086; Aldehyde_dehydr.
                                                                                          65
                                                                                                                                                                                                                                                                                                                                                               Euteleost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9PT69
Q9PT69;
Q9PT69;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EPHRIN-B3 PRECURSOR.
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IATSDGTMDGIETLOGGVCETKGMKVTLKV---GOSPNGATP-PRRPSSAGKDSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --HWKCLRMKVFVCCASTSHSGEKPVPTLPQFT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                 -- PGPRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
4BB0FA39D4C22DCD CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EHLPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEHYDR_GLU; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 164.5; DI
Pred. No. 8e-09.
; Mismatches
                         SSGVGPGAGPGGGGA--EQYVLYMVSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINVLEDFEGENPQVPKLEKSISGTSPKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 F
35913 MW;
                                                                                                                             SGEK PVPTLPQFTMGPNVK - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 12.6%;
Similarity 26.6%;
63; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1
PROSITE; PS00687; ALDEHYDE_PROSITE; PS01299; EPHRIN; 1
                                                                                                                                                                                -LAVGIAFFLM
                                                                                                                                                                                              KEEMSSCSILRTPNL --
  ILLIFLVDLLGITAT
                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
TISSUE=EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISTPTHNL-
                                                                                                                                                                               LP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
SIGNAL
SEQUENC
                                                                                                                                                                                                                                             14
12
                                                                                                                                                                                                      213
                         68
                                                  65
                                                                           113
                                                                                                                                                     158
                                                                                                    105
                                                                                                                             173
                                                                                                                                                                              222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
                                                                                                                                                                                                                                            RESULT
Q9PT69
                                                  qq
                                                                                                  П
                                                                                                                                                                                                                                                                   qa
                                                                                                                                                                                                      qq
```

```
Euteleostomi;
dae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YEYYKVYMVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGYRTCNASOGFKRWECNRP----HAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNGSLEGLNNQEGGVCQTKTMKILMKVGQDPNSAGLPRSTDPTKRPEQEAGTNGKSSTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- NTPLLNCAKPDQDVKFTIKFOEFSPNLWGLEFOKNKDYYVIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --WKCLRMKVFVCCASTSHSGEKPVPT----LPQFTMGPNVKINV--
                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                        333;
                                 OgPUJ4;
OgPUJ4;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EPHRIN-B2 PRECURSOR.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Phasianidae; NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                               ephrin-B2.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
                                                                                                                                                                                                                                                                                                                     POTENTIAL.
EPHRIN-B2.
4C28E8CB211B7783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LEDFEGENPQVPKL-EKSISGTSPKREHLPLAVGIAFFLMTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | | | | | : | : | - - EVALFAGIASGCIIFI
                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                      Score 162.5; DB 13
Pred. No. 1.3e-08;
; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 PFVKDHSGSSTDGSKAGHSSILGS--
                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                    27 P
333 E
36761 MW;
                                                                                                                                                                                SEQUENCE FROM N.A.
Menzel P., Pasquale E.B.;
"Coding sequence of chicken epsubmitted (AUG-1999) to the ENEMBL; AF180729; AAD53948.1;
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                     th 12.5%; Similarity 27.1%; 61; Conservative 29
                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQADSCAIRKD----
                                                                                                                                                                                                                                                                                                                                 28
333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 PTHNLH----
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
CHAIN
                          09PUJ4
15
                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
RESULT
Q9PUJ4
                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
```

9

2002, 10:52:33 completed: July 13, ne: 463 sec Search Job tim

time:

qq

õ

QY

qq

ò

ga

Qγ

```
GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
             Copyright
```

- protein search, using sw model OM protein

July 13, 2002, 10:45:35; Search time 24.34 Seconds (without alignments) 378.605 Million cell up Run on:

US-09-733-756-2 1301 1 MAAAPLLLLLLLVPVPLLPL.....REHLPLAVGIAFFLMT Title: Perfect score: Sequence:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	2797 homo sap	8545 mus mus	snw	3921 homo	79727 brach	52802 gallu	52803 ho	8543 mus r	760	8542 mus mus	2804 qal	9728 brachyd	0827	2794 xenop	2793 mus muscu	2798	7553 rattu	576	5393 mus m	799 hom	2800 mus m	98172	73874 brach		309	2796	12	•—	Q12906 h interleuk	Q9cyd3 mus musculu	09jil3 rattus norv	11370 mus mu	07247 dros
	QI	FA3_HUMA	EFA3_MOUSE	EFA2_MOUSE	EFA2_HUMAN	EFA2_BRARE	<.	EFA5_HUMAN	٦	EFA5_RAT	- 1	EFA5_CHICK	EFA5_BRARE	EFA1_HUMAN	EFA1_XENLA	EFA1_MOUSE	EFA4_HUMAN	EFA1_RAT	EFB3_HUMAN	1	- 1	7	<u>, </u>	2		,	긥	7	POLG_POL32	ILF3_HUMAN	Σ	ILF3_RAT	ENV2_MOUSE	_
	DB		Н	٦	Н	-	-	_	, ,	П	-	-	, ,	H	-	- -1	, -	_	-	-	Н.	-	-	.	4		7	-1	-1		-	-	-	7
	Length	238	8	209	4	9	0	$^{\circ}$	$^{\circ}$	$^{\circ}$	0	$^{\circ}$	\sim	0	_	\circ	0	\circ	₹	*	333	\sim	₩.	m -	-	327	**	33	2206	œ.	$\overline{}$	_	432	10
80 U	Match	100.	4.	m.	ω.	~;	Ċ.	-i	_;			_;	Ċ	<u>.</u>		т т	ф.	ζ.	<u>.</u>	<u>.</u>	<u>~</u>	<u>.</u>				<u>.</u>					_	_	_	
	Score	3	v	{**}	£7}	(N	4.2	•	4	14.	4	•	ന	<u>м</u>		37		เดา	<u> </u>	17		71.	48 	14		13		22.	σ,	88.5	Φ	ر	82.5	7
Result	i		7	m ·	4	Ŋ	9	7	Φ,	ه <u>'</u>	10	11	12	13	14	15	16	17	8 7	19	20	21	22	5.7	77 (25	97	77	28	29	30	3.1	3.2	

	Q10462 caenorhabdi	Q9z1x4 mus musculu		P38159 homo sapien		_		P48431 homo sapien	-	P05315 solanum tub	P13677 drosophila
SOX2_MOUSE	CAHX_CAEEL	ILF3_MOUSE	SN24_HUMAN	ROG_HUMAN	ENV_HV1MN	BGAL_ECOLI	HXBD_HUMAN	SOX2_HUMAN	SOX2_SHEEP	CHIT_SOLTU	KPC2_DROME
1	_	-	-	-	ч	Ч	-4		-	-	-
319	334	911	1647	391	856	1023	284	317	320	328	700
6.3	6.3	6.2	6.2	6.1	6.1	6.0	0.9	9.0	0.9	0.9	0.9
82	82	81	81	79.5	79	78.5	78	78	78	78	78
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

--

.IS

6 - 2

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r commercial
ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
tions on it
                                                                                                                                                                 120
                                                                                                                                                                                     120
                                                                                                                                                                                                         180
                                                                                                                                                                                                                              180
                                                                                                                          9
                                                                                                                                              9
                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sis.";
                                                                                                                       nchor
                                                                                                                                                              SHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ephrin-A3 (EPH-related receptor tyrosine kinase ligand 3) (LERK-3)
(EHK1 ligand) (EHK1-L) (Fragment).
EFNA3 OR EPLG3 OR LERK3 OR EPL3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL of the European Bioinformatics Institute. There are no restrictionse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.chor send an email to license@isb-sib.ch).
         .) (POTENTIAL .) (POTENTIAL .) (POTENTIAL .)
                                                                                                     0
                                                                                 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=129;
MEDLINE=98126446; PubMed=9465306;
Cerretti D.P., Nelson N.;
"Characterization of the genes for mouse LERK-3/Ephrin-A3 mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 conservation of intron/exon structure.";
Genomics 47:131-135(1998).
                                                                                Length
                                                                                                    Indels
                                                                                                                                                                                                        KFSEKFQRYSAFSLGYEFHAGHEYYY1STPTHNLHWKCLRMKVFVCCAST
                                                   CRC64
        N-LINKED (GLCNAC....
N-LINKED (GLCNAC....
N-LINKED (GLCNAC.....
MISSING (IN REF. 2)...
                                                                               Score 1301; DB 1;
Pred. No. 2.8e-115;
                                                                                                    ;
0
                                                                                                   Mismatches
                                                                                                    0;
                                                 .,
Μ
                                                                              100.0%;
larity 100.0%;
Conservative (
38
67
100
74
26350 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U92885; AAC39961.1;
U90666; AAB50241.1;
MGI:106644; Efna3.
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001799;
                                                                                          1 Similarity
238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090
        38
67
100
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; U90666; AA
                                                                                                                                                                                                                                                                                                                                5217;
                                                 238
                                                                                                                                                                                                                                                                                                                    EFA3_MOUSE
008545; 0552
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U906
MGD; MGI:1
InterPro;
      CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                              Query Match
Best Local S
Matches 238
                                                                                                                                                                                                                                                                                                 RESULT 2
EFA3_MOUSE
                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                61
                                                                                                                                                                                                       121
                                                                                                                                                                                                                           121
                                                                                                                                            q
                                                                                                                                                               οχ
                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                ò
```

```
112
                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                       10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                    --GPGGGAEQYVLYMVNLSGYRTCNASQ
                                                                                                                                                                                                                                                                                                                           GPI-anchor
                                                                                                                                                                                                                                                                       LRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ
                                                                                                                                                                                                                                                                                                                                                                               FVCCASTSHSGEKPVPTLPGFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP
                                                                                                                                                                                                                                                                                                                                                                                             mi;
Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase ligand
                                                                                (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit "cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases J. Biol. Chem. 270:3467-3470(1995).
                                                                                                                                                                                                                                             .;
&
                                                                                                                                                                                                                    187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a developmentally tyrosine kinases."
                                                                                                                                                                                                                    Length
                                                                                                                                                          -> W (IN REF. 2).
CCE4915751760743 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ру
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; |
hi; Muridae;
                                                                             W-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EFA2_MOUSE STANDARD; PRT; 209 AA. P52801; 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Ephrin-A2 precursor (EPH-related receptor tyrosine (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L). EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane
                                                                                                                                                                                                                                           .
9
                                                                                                                                                                                                                    ; DB 1;
1.3e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential). SIMILARITY: BELONGS TO THE EPHRIN FAMILY
                                                                                                                                                                                                                  Score 963; DB Pred. No. 1.3e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the
                                                                              N-LINKED (
N-LINKED (
Y -> I (IN
EQ -> DR (
RT -> QP (
Y -> W (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=SWISS WEBSTER; TISSUE=Brain;
MEDLINE=95007776; PubMed=7522971;
Cheng H.J., Flanagan J.G.;
"Identification and cloning of ELF-1,
ligand for the Mek4 and Sek receptor
Cell 79:157-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of ELF-1, receptor
                                                                                                                                                                                                                                                                                     #RREGYTVQVNVNDYLDIYCPHYNSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=95181289; PubMed=7876076;
                                                                                                                                                                                                                                             3;
                                                                                                                                                                             ĭ,
                                                                                                                                                                                                                 74.0%;
ilarity 91.3%;
Conservative
                            ~~
Pfam; PF00812; Ephrin; 1.
ProDom; PD002533; Ephrin; 1
PROSITE; PS01299; EPHRIN; 1
Glycoprotein; GPI-anchor.
                                                                                                                                                                           21171
                                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
                                                                                24
41
49
19
47
78
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLMTFLAS
                                                                                                                                                                               AA;
                                                                                                                                                                                                                                l Similarity
178; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                24
41
49
19
19
46
78
                                                                                                                                                                                                                                                                                                                                                                                                                                   LAVGIAF
                                                                             CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
                                                                                                                                                                                                                   Query Match
Best Local S
Matches 178
                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFA2_MOUSE
                                                                                                                                                                                                                                                                                                 Ч
                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                            104
                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                  224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
               ga
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID
                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
```

.rsp

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     á
                                               is in no way
for commercial
ib.ch/announce/
        collaboration
                                                                                                                                                                                                                                                                                                                                                                                7;
                      outstation
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            YTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (9
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Ep13),
(EPLG6);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
                                                                                                                                                                                                                                                                       AL)
                                                                                                                                                                                            1; 1.

N; 1.

POTENTIAL.

EPHRIN-A2.

N-LINKED (GLCNAC. .) (POTENTIAL)

N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCO
This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imposified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E., Adamson A.W.,
Ramirez M., Stilwage
L., Poundstone P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleos
i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98126446; PubMed=9465306;
Cerretti D.P., Nelson N.;
"Characterization of the genes for mouse LERK-3/Ephrin-A3
mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2
conservation of intron/exon structure.";
Genomics 47:131-135(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinas
                                                                                                                                                                                                                                                                                                                                                                                                           AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFA2_HUMAN STANDARD; PRT; 213 AA. 043921; 076020; 15-DEC-1998 (Rel. 37, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Ephrin-A2 precursor (EPH-related receptor tyrosine (LERK-6) (HEK7-ligand) (HEK7-L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamerdin J.E., McCready P.M., Skowronski
Burkhart-Schultz K., Gordon L., Kyle A.,
Phan H., Velasco N., Garnes J., Danganan
                                                                                                       EMBL; U14941; AAA53636.1; -.
EMBL; U14752; AAA68520.1; -.
MGD; MGI:102707; Efna2.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Sign SIGNAL 1 20 E CARBOHYD 38 38 N CARBOHYD 170 I70 N CARBOHYD 170 I70 N CARBOHYD 184 184 N SEQUENCE 209 AA; 23586 MW;
                                                                                                                                                                                                                                                                                                                                                     33.6%;
Similarity 50.5%;
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : |: |
173 LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FA2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                                                                                                                                                                                                                                                         ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113
                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
  E
                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
                                                                                                                                                                                                                                                                                              GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EGYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHAPHSPIKESEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHA4
                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
                   Lucas S.
                                                                                                                                                                                                     gene
                                                                                                                       SEQUENCE FROM N.A.

TISSUE=Brain;

MEDLINE=99045414; PubMed=9826538;

Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;

Aasheim H.C., Pedeutour F., Grosgeorge J., Logtenberg T.;

"Cloning, chromosal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2.";

Biochem. Biophys. Res. Commun. 252:378-382(1998).

-!- SUBGNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPH EPHA5.

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-an (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                      Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 213;
  Noila J., Liu S., Attix C. Coefield J., Duarte S., Li Tronmiller B., Arellano A. Trong S., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Christensen M., Georgescu A., Avila J., Liu S., Attix C Trankheim M., Amico-Keller G., Coefield J., Duarte S., I Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Carrano A.V.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ???
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Signal.
    POTENTIAL.
    EPHRIN-A2.
    N-LINKED (GLCNAC. . .)
    N-LINKED (GLCNAC. . .)
    N-LINKED (GLCNAC. . .)
    R -> A (IN REF. 3).
    RA -> PP (IN REF. 3).
    AA -> RR (IN REF. 3).
    AA -> RR (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed. No. 5e-3
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U92896; AAC39577.1; -.
EMBL; U92893; AAC39577.1; JOINED
EMBL; U92894; AAC39577.1; JOINED
EMBL; AC004258; AAC04896.1; -.
EMBL; AJ007292; CAA07435.1; -.
MIM; 602756; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Sign SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 F 30 A 23878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
42
174
188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
42
174
188
6
25
29
213 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F Mar
Local Sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
```

60-

ns

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                        CREATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                   GRADED
                                                                                                                                                                                                                                                                                                                                                 a GPI-anchor
                                                                                                                                                                                                                                                                   and
                                                                                                                          comi;
                                                                                                                                                                                                                                                                                                                                                       (Potential).

TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.

DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF
DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT

EXPRESSED THROUGHOUT THE MIDBRAIN INCLUDING THE REGION OF THE
PRESUMPTIVE TECTUM. AT LATER STAGES IT IS EXPRESSED IN A GRADI
FASHION THROUGHOUT THE TECTUM.

SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 LGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -POPHSRMERYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                 growth
the
                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase liga (LERK-6) (ELF-1) (ZFEPHL3).
EFNA2 OR EPLG6 OR LERK6.
Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosta Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariop)
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurogenesis; Glycoprotein; GPI-anchor;
POTENTIAL.
EPHRIN-A2.
N-LINKED (GLCNAC. . .) (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development 124:655-664(1997).
-!- FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE OF THE RETINO-TECTAL MAP.
                                                                                                                                                                                                                                       B., Drescher U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                    axon
                                                                                                                                                                                                                                                                                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Attached to the membrane by
                                                                                                                                                                                                                                                                                шар
                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=97195707; PubMed=9043080;
Brennan C., Monschau B., Lindberg R., Guthrie B.,
Bonhoeffer F., Holder N.;
"Two Eph receptor tyrosine kinase ligands control
be involved in the creation of the retinotectal ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 426; DB 1;
Pred. No. 4.9e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ed. No. 4.96
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STPTHNLHWK-CLRMKVFVCCASTSHSGEKPVPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y09668; CAA70863.1; -. ZFIN; ZDB-GENE-990415-66; efna2 InterPro; IPR001799; Ephrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogen SIGNAL 1 16 PO CHAIN 17 195 EP CARBOHYD 32 32 N-SEQUENCE 195 AA; 22688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.7%;
illarity 52.3%;
Conservative 2.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                               <del>-</del>:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Öγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

EMBL; L40932; AAC42229.1; -...
EMBL; L40932; Aptrin.
Prodom; PRO0812; Ephrin.
Probom; PRO1347; EPHRIN.
PROSITE; PS01299; EPHRIN.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
                                                                                                                                                                                                                                                                                                                                                                                                        Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.; "Complementary gradients in expression and binding of ELF-1 and Mek4 in development of the topographic retinotectal projection map."; Cell 82:371-381(1995).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA3, EPHA4 AND EPHA5 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
(LERK-6) (ELF-1).
EFNA2 OR EPLG6 OR LERK6 OR ELF1.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAPLILILILLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
POTENTIAL.
EPHRIN-A2.
N-LINKED (GLCNAC. . .) (POTENTIAL).
49 MW; 8FABIAE5E45EED96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TECTUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Potential).
TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT ACROSS T
BEING MORE STRONGLY EXPRESSED AT THE POSTERIOR POLE.
SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 421; DB 1; 1
Pred. No. 1.5e-32;
); Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=95360981; PubMed=7634327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.4%;
|larity 47.5%;
|Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; GPI-anchor; SIGNAL 1 22
CHAIN 23 200
CARBOHYD 36 36
CARBOHYD 161 161
CARBOHYD 175 175
SEQUENCE 200 AA; 23049 M
STANDARD;
                                                                                                                                                                                                                              Eukaryota; Metazoa;
Archosauria; Aves; l
Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPHYEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>'</del>-
```

Tue

```
E
a
```

```
MEDLINE-20069483; PubMed=10601038;

MEDLINE-20069483; PubMed=10601038;

A Davy A., Gale N.W., Murray E.W., Klinghoffer R.A., Soriano P.,

Fourstein C., Robbins S.M.;

"Compartmentalized signaling by GPI-anchored ephrin-A5 requires the rompartmentalized signaling by GPI-anchored ephrin-A5 requires the Fyn tyrosine kinase to regulate cellular adhesion.";

"Compartmentalized signaling by GPI-anchored ephrin-A5 requires the ryn tyrosine kinase to regulate cellular adhesion.";

"CompartmentalizeD SIGNALING WITHIN A CAVEOLAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE.

"COGNATE RECEPTOR TYROSINE KINASE."

"COGNATE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AND EPHB1.

"COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOMAINS."

"MICRODOMAINS."

"MICRODOMAINS."

"MICRODOMAINS."

"MICRODOMAINS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=97392664; PubMed=9245480;
Kozlosky C.J., Vandenbos T., Park L.S., Cerretti D.P., Carpenter M.K.;
"LERK-7: a ligand of the Eph-related kinases is developmentally regulated in the brain.";
Cytokine 9:540-549(1997).
                                                                                                                     5
                                                                                                                       gand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                        ığ
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95267434; PubMed=7748564;
Winslow J.W., Moran P., Valverde J., Shih A., Yuan J.Q., Won Tsai S.P., Goddard A., Henzel W.J., Hefti F.;
"Cloning of AL-1, a ligand for an Eph-related tyrosine kinas receptor involved in axon bundle formation.";
Neuron 14:973-981(1995).
                           01-OCT-1996 (Rel. 34, Created)
16-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase (LERK-7) (AL-1).
EFNA5 OR EPLG7 OR LERK7
                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                   Eutel
                                                                                                                                                                                            Craniata; Vertebrata; P
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE EPHRIN FAMILY
                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U26403; AAB60377.1;
                    STANDARD;
              EFAS_HUMAN STANDARD
P52803;
01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, L
16-OCT-2001 (Rel. 40, L
                                                                                                                                                                                                                                                                                                                                                                                                                                FROM N.A
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601535;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
HUMAN
                                                                                                                                                                        DT
DE
DE
GN
```

Signal

.) (POTENTIAL)

POTENTIAL. EPHRIN-A5. N-LINKED (GLCNAC.

20 228 37

1 21 37

CHAIN CARBOHYD

Polymorphism SIGNAL

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n no way
commercial
                                                                                                                   11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions on it is as its content is in ed. Usan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;

Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;

Thistinct and overlapping expression patterns of ligands for generated receptor tyrosine kinases during mouse embryogenesis.";

EDP. EDP. Biol. 179:382-401(1996).

- I. FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.

INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF ITS COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY OF THE FYN TYROSINE KINASE (BY SIMILARITY).

- I. SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IT IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE

MICRODOMAINS (BY SIMILARITY).

- I. ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

- I. SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPI-ANCHOR IT
                                                                                                                                                                     ---VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                                                                                                                                    FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
                                                                                                                                                   LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                   NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                    --LLAI
                                                                                                                                                                                                                                                                                                                                                   -GEN-POVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata; Euteleostomi
                                                                                                                  47;
                                                                                                                                                                                                                                                                                                    228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Euthería; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase
                                                                                                                                                                                                                                                                                                                                                                                   -PSR-
                                                                                    Length
                                                                                                                   Indels
N -> K (IN DBSNP:469062).
/FTId=VAR_012035.
6893B1CCACFF3F57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFA5_MOUSE STANDARD; PRT; 228 AA.
008543; 008544;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
EPhrin-A5 precursor (EPH-related receptor tyrosine (LERK-7) (AL-1).
                                                                                 ore 415.5; DB 1;
ed. No. 5.7e-32;
Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                    --VEDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI-
                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=97060319; Pubmed=8903354
                                                                                                                 37;
                                   MW.
                                                                                 31.9%;
larity 39.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                   LPQFTMGPNVKINVLEDFE---
                                   26297
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit modified and this st
                                    AA;
                                                                                               Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 LLFLLAML 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090
55
                                                                                                                                                                                                                                                                                                                                                                                                                   AFFLMTFL
                                                                                 Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
                                   SEQUENCE
                                                                                                                                                                                                                                                   EDS
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 8
MOUSE
                                                                                                                                                                                                                                                                                  126
                                                                                                                                                   ထ
                                                                                                                                                                                   9
                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                  118
                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
EFA5_M
 FT
FT
SO
                                                                                                                                                                                  ga
                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                   ò
                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                  Signal
                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=SPRAGUE-DAWLEY;
Li Y.Y., McTiernan C.F., Feldman A.M.;
Li Y.Y., McTiernan C.F., Feldman A.M.;
"LLERK7, rat ligand for Eph-related receptor tyrosine kinase.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY FUNCTION ACTIVELY TO STIMULATE AXON FASCICULATION.
INDUCES COMPARTMENTALIZED SIGNALING WITHIN A CAVEOLAE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                    --VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                         LLAI
                                                                                                                                                                                                                                                                                                        FSEK
                                                                                                                                                                                                                                                                                                                                                     -- CCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                  -GEN-PQVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi
Murinae; Ra
                                                                                                                                                                                                                                   ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                 47
                                                                                                  GPI-anchor
                                                                                                                                                                                                                                                                                                    NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSP1K
                                                                                                                                                                                                                                                                                                                                                               Yuan J.Q., Wong
Beck K.D., Caras
tyrosine kinase
                                                                                                                                                                                                           Length 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase (LERK-7) (AL-1).
EFNA5 OR EPLG7 OR LERK7.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                          -PSR-
                                                                                                                                                                                                                                 Indels
                                                                                                                                EPHRIN-A5.
N-LINKED (GLCNAC. . .) (PO'MISSING (IN SHORT ISOFORM)
85439F5337420022 CRC64;
                                                                                                  Glycoprotein;
                                                                                                                                                                                                       Score 414.5; DB 1;
Pred. No. 7.1e-32;
; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                     FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=SPRAGUE-DAWLEY;
MEDLINE=95267434; PubMed=7748564;
Winslow J.W., Moran P., Valverde J., Shih A.,
Tsai S.P., Goddard A., Henzel W.J., Hefti F.,
"Cloning of AL-1, a ligand for an Eph-related receptor involved in axon bundle formation.";
Neuron 14:973-981(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                      --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI
                                                                                                                         POTENTIAL.
                                                         PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                               36;
                                                                                                                                                                     MW;
EMBL; U90664; AAB50239.1; -. EMBL; U90665; AAB50240.1; -. MGD; MGI:107444; Efna5. InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1.
                                                                                                                                                                                                       th 31.9%;
Similarity 39.5%;
98; Conservative
                                                                                                                                                                      26339
                                                                                                                                                                                                                                                                                                                                                                                                 LPOFTMGPNVKINVLEDFE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                 228
37
189
                                                                                                                     20
                                                 Ephrin;
                                                                                                                                                                       AA;
                                                                                                                                             37
163
28 7
                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                              AFFLMTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLFLLAML
                                                                                                           Alternative
SIGNAL
                                                                                                                                            CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                       Ouery Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFA5_RAT
P97605;
                                                                                                                                                                                                                                                                                                                            EDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                             229
                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218
                                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  Ω
                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal
                                                                        AND
                                                                                                                                                                                            HEART, PLACENTA AND LUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
MEMBRANE MICRODOMAIN WHEN BOUND TO THE EXTRACELLULAR DOMAIN OF COGNATE RECEPTOR. THIS SIGNALLING EVENT REQUIRES THE ACTIVITY COTHE FYN TYROSINE KINASE (BY SIMILARITY).

SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA3 AN EPHB1 (BY SIMILARITY).

SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR IS COMPARTMENTALIZED IN DISCRETE CAVEOLAE-LIKE MEMBRANE MICRODOMAINS (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, PLACENTA AND LUNSIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NSSGVGPGAGPGGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GEN-POVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PSR----LLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFA4_MOUSE STANDARD; PRT; 206 AA.
008542; 055218;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-A4 precursor (EPH-related receptor tyrosine kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 FQLFTPFSLGFEFRPGREYFYISSAIPDNGRRSCLKLKVFVRPTNSCMKTIGVRDR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Neurogenesis; Glycoprotein; GPI-anchor; 0 POTENTIAL. 8 EPHRIN-A5. 7 N-LINKED (GLCNAC. . .) (POTENTIAL) 6358 MW; 855985532D580022 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1e-32;
les 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 414.5;
Pred. No. 7.1e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LERK-4).
EFNA4 OR EPLG4 OR LERK4 OR EPL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
228
37
26358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U69279; AACO5801.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.9%;
larity 39.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPQFTMGPNVKINVLEDFE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Developmental protein SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
37
228 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AFFLMTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | : |
LLFLLAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 EDS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFA4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
```

.rsp

us-09-733-756-2

~

Tue

```
LT 12
_BRARE
EFA5_BRARE
P79728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 EDS-
                                                                                                                                 kinases.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                 Galius
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
EFA5_BF
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                           way
                                                                                                                                                                              collaboration
                                                                                                                                                                                                                    for commercial ib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                       EMBL outstation trictions on it
                                                                                                                                          (By
                                                                                                                                                                                                             000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPHYN. 67
                                                                                                                                                                                                                                                                                                                                                                                                   (IN REF.
                               nesis.";
                                                                                                                                         anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gand 7)
                                                                                                   (Epl3),
(EPLG6):
                                                                                                                                                                                                           in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PGPPEGPETFALYMVDWSGYEACTAEGANAFQRWNCSMPFAPFSPVRFSEK
                                                                                                                                                                                                                                                                                                                                                                              (AL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTI?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97060319; PubMed=8903354;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for
Eph-related receptor tyrosine kinases during mouse embryoger
Dev. Biol. 179:382-401(1996).
                                                                                                                                                                                                                                                                                                                                                                                     ATTACHMENT SITE (POTENTI
ATTACHMENT SITE (POTENTIAL
-> MLLRLGLIYPPTRPPAPPGPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNA - - SQGFKRWECNRPHAPHSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCC--ASTSHSGEKPV
                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EME the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imposified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sjorsend an email to license@isb-sib.ch).
                                                                                                                                         GPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor tyrosine kinase li
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 206
                                                                                                 LERK-3/Ephrin-A3
LERK-6/Ephrin-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                          đ
                                                                                                                                        þλ
                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64
                                                                                                                                       to the membrane
                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
EPHRIN-A4.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
CELL ATTACHMENT SIT
                                                                                                                                                                                                                                                                                                                                                                                                                           43501971DD1C6EA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 1;
1.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFAS_CHICK STANDARD; PRT; 228 AA. P52804; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Ephrin-A5 precursor (EPH-related receptor tyre (LERK-7) (RAGS protein).
                                                                                                                                                          FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.5%; Score 410; DE larity 47.4%; Pred. No. 1.76 Conservative 18; Mismatches
                                                                                    Cerretti D.P., Nelson N.;
"Characterization of the genes for mouse mouse LERK-4/Ephrin-A4 (Ep14), and human conservation of intron/exon structure."; Genomics 47:131-135(1998).
                                                                                                                                                          TO THE EPHRIN
                                                                                                                                                                                                                                                    EMBL; U90663; AAB50238.1; -.
EMBL; U92890; AAC39962.1; -.
EMBL; U92889; AAC39962.1; JOINED.
MGD; MGI:106643; Efna4.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
                                                                             MEDLINE=98126446; PubMed=9465306
                                                                                                                                                                                                                                                                                                             PRINTS; PR01347; EPHRIN.
Probom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                           22861 MW;
                                                                                                                                                                                                                                                                                                        purin; 1.
EPHRIN.
                                                                                                                                                similarity).
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                               206
33
98
43
                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
83; Conser
                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                               226
333
41
1
                                                                                                                                                                                                                                                                                                                                                                                                                          206
                                                                                                                                                                                                                                                                                                                                            Glycoprotein; SIGNAL
                                                                   STRAIN=129
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ន
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFA5_
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC
DT
DT
```

ò

q

DE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinases.;
Cell 82:359-370(1995).
-!- FUNCTION: INDUCES GROWTH CONE COLLAPSE AND REPULSION OF RETINAL GANGLION CELL AXONS.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN A GRADED FASHION ACROSS THE TECTUM BEING MORE STRONGLY EXPRESSED TOWARDS THE POSTERIOR POLE.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ephrin-A5 precursor (EPH-related receptor tyrosine kinase ligand (LERK-7) (AL-1) (2FEPHL4).
EFNA5 OR EFNA5B OR ALI OR EPLG7 OR LERK7.
Brachydanio rerio (2ebrafish) (2ebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                               SEQUENCE FROM NO...
TISSUE=Posterior tectum;
MEDLINE=95360980; PubMed=7634326;
MEDLINE=95360980; JubMed=7634326;
MEDLINE=95360980; PubMed=7634326;
MEDLINE=95360980; PubMed=7634326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL) 56D8E4FBDECF18AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "In vitro guidance of retinal ganglion cell axons by RAGS, tectal protein related to ligands for Eph receptor tyrosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .31.1%; Score 404.5; DB 1; 49.1%; Pred. No. 6.2e-31; tive 29; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Or send au.

EMBL; X90377; CAA62027.1; -.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Developmental protein; Neurogenesis; Glyconelopmental protein; Glyconelopmental protein; Glyconelopmental 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26206 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 79; Conser
                                                                                                                                                                                                       NCBI_TaxID=9031;
```

.,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.
                                                                                                                                                                                                  CREATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                              LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MARGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPHY · 66
                                                                                                                                                                                                                                                                       IN OF S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
,
Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                              GPI-anchor
                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSEK
                                                                                                                                                                                                                                      (Potential).

TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN THE EMBRYO.

DEVELOPMENTAL STAGE: EXPRESSED IN THE PRESUMPTIVE MIDBRAIN OF

DEVELOPING EMBRYOS FROM THE SIX-SOMITE STAGE. BY 24 HOURS IT

STRONGLY EXPRESSED IN THE MIDBRAIN CAUDAL TO THE PRESUMPTIVE

TECTUM. AT LATER STAGES IT IS MAINTAINED AT THE POSTERIOR MAIOF THE TECTUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligation (LERK-1) (Immediate early response protein B61) (Tumor necrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLVPVPL-LPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VPEERTERYVLYMVNYDGYSTCDHTAKGFKRWECNRPHSPNGPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein; GPI-anchor
                                                                                                                                                                             FUNCTION: CONTROL AXON GROWTH AND MAY BE INVOLVED IN THE OF THE RETINO-TECTAL MAP.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-
                                                                                                              D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228;
                                                                                                              Drescher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                          axon
                                                                                                                                                       map in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                      Brennan C., Monschau B., Lindberg R., Guthrie B., Bonhoeffer F., Holder N.; "Two Eph receptor tyrosine kinase ligands control be involved in the creation of the retinotectal ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. 74B3406C05418E6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.5%; Score 397; DB 1; 47.8%; Pred. No. 3.1e-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE EPHRIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; if Ephrin, — Promain Pro0812; Ephrin, — PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1. PROSITE; PS01299; EPHRIN; 1. 20 POTENTIAL. — 20 POTENTIAL. — 1 20 POTENTIAL. — 1 20 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y09669; CAA70864.1; -. ZFIN; ZDB-GENE-980526-186; efna5b. InterPro; IPR001799; Ephrin.
                                                               SEQUENCE FROM N.A.
TISSUE=Embryo;
MEDLINE=97195707; PubMed=9043080;
        Actinopterygii; Neopterygii; Tele
Cypriniformes; Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MΨ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 .
228
37
26595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Similarity
77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
37
228 A
                                                                                                                                                                  zebrafish.";
Development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFA1_HUMAN P20827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFA1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                     RESULT
       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Π
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC
DT
DE
DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in no way
commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its conversed by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elk: isolation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                    induced by
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95140419; PubMed=7838529;
Kozlosky C.J., Maraskovsky E., McGrew J.T., Vandenbos T.,
Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III.
Cerretti D.P., Beckmann M.P.;
"Ligands for the receptor tyrosine kinases hek and elk: isolation of concogene 10:299-306(1995).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor-
-!- INDUCTION: BY TNF-ALPHA AND INTERLEUKIN-1 BETA.
-!- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.
                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - POAHVNPOEKRLAADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 205;
                                                                                                               Ношо
                                                                                                                                                                                                                                                                        endothelium is ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHRIN-A1.
N-LINKED (GLCNAC. . .) (Poster of the control of the co
                                                                                     Vertebrata; I
; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 390; DB Pred. No. 1.3e 1; Mismatches
                                                                                                                                                                                         MEDLINE=91042512; PubMed=2233719;
Holzman L.B., Marks R.M., Dixit V.M.;
"A novel immediate-early response gene of
cytokines and encodes a secreted protein."
Mol. Cell. Biol. 10:5830-5838(1990).
                                                                                   Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225
   ein 4).
TNFAIP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEGENPQVPKLEKS ISGTSPKREHLPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- PEVRVLHSIGHSAAPRL -- FPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.0%; Sollarity 41.8%; Poconservative 21;
factor, alpha-induced protein
EFNA1 OR EPGL1 OR LERK1 OR TNI
                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23771 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001799; Ephrin. Pfam; PF00812; Ephrin; 1. PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; 1. PROSITE; PS01299; EPHRIN; 1. Glycoprotein; GPI-anchor; Sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M57730; AAA58388.1;
PIR; A36377; A36377.
MIM; 191164; -.
InterPro; IPR001799; Ephr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
26
                                                     (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26
205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 87; Conser
                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     -ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                                                                              GPI
                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
```

9

RESULT

rsp.

-756-2

```
мау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL outstation trictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPHRIN-A1.

N-LINKED (GLCNAC. . .) (POTENTIAL).

TPPPVNVHTPRSHIQSDEPEVPLPGVMKSVAGNSAAPGTPC
TLYGLLLAALLLRL -> SE (IN ISOFORM A').

1B3A508E0A7B872E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPEVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPHA1
                                                                                                                                                                                                                    stomi;
e;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||
RTYYY
                                                                                                                        gand
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPHA4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216;
                                                                                                                                                                                                                    Euteleos
Pipidae
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97000306; PubMed=8843391;
Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A. Weinstein D.C., Rahman S.M., Ruiz J.C., Hemmati-Brivanlou A. "Embryonic expression of eph signalling factors in Xenopus."
Mech. Dev. 57:133-144(1996).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, I EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO SIMILARITY).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -OSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal
                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine ki
(LERK-1) (XELF).
EFNAI OR EPGLI OR ELF.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SGRTTPPPVNVHTPRSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 375.5; DB 1 Pred. No. 3.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE EPHRIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.
1.
Alternative
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ж
Ж
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.9%;
41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31204; AAA74485.1; -
EMBL; U31205; AAA74486.1; -
InterPro; IPR001799; Ephrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01347; EPHRIN. ProDom; PD002533; Ephrin; PROSITE; PS01299; EPHRIN; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24755
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephrin; 17; EPHRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISKPIHYHGETCMRLRVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
216
36
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PKLEKSISGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPGVMKSVAGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
36
162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                          FT TW DDR REAL DDR RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

RESULT

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      (By
                                                                                                                                                                                                                                                                                                                                  MEDLINE=97060319; PubMed=8903354;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
Flenniken A.M., Gale N.W., Yancopoulos G.D., Wilkinson D.G.;
"Distinct and overlapping expression patterns of ligands for
Eph-related receptor tyrosine kinases during mouse embryogenesis.";
Dev. Biol. 179:382-401(1996).
-!- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EPHA2, EPHA4,
EPHA5, EPHA6 AND EPHA7. ALSO BINDS WITH LOW AFFINITY TO EPHA1.
                                                                                                           mi;
Mus
EFA1_MOUSE STANDARD; PRT; 205 AA.
P52793; P97331;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ephrin-Al precursor (EPH-related receptor tyrosine kinase ligand (LERK-1) (Immediate early response protein B61).
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                              ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=BALB/C;
Morris J.C., Clarletta A., Morris G.E., Giannotti J., Caruso Hammett D.J., Finnerty H., Turner K., Wood C.R.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                             MEDLINE=95405853; PubMed=7675446; Takahashi H., Ikeda T.; "Molecular cloning and expression of rat and mouse B61 gene: implications on organogenesis."; Oncogene 11:879-883(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.
Signal.
POTENTIAL.
EPHRIN-A1.
N-LINKED (G
H -> Y (IN
Q -> E (IN
N -> K (IN
T -> S (IN
I -> T (IN
S -> T (IN
Y -> S (IN
Y -> H (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D38146; BAA07344.1; -.
EMBL; U26188; AAA67563.1; -.
EMBL; U90662; AAB50237.1; -.
MGD; MGI:103236; Efnal.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
Glycoprotein; GPI-anchor; Sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
206
74
74
79
81
91
112
113
115
115
115
115
115
115
115
115
                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
74
79
81
91
112
115
115
115
115
115
115
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
SIGNAL
                                                                                                                                                                    STRAIN-ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
```

```
26; Gaps
                                                             Query Match

28.7%; Score 374; DB 1; Length 205;
Best Local Similarity 38.7%; Pred. No. 4e-28;
Matches 86; Conservative 23; Mismatches 87; Indels ...
204 S -> T (IN REF. 1).
23802 MW; 5A8F3A6E2091E868 CRC64;
                                                                                                                                                         -FEGENPOVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
                                                                                                                                                                   204
205 AA;
CONFLICT
SEQUENCE
                                                                                                                                                           198
FT
SQ
                                                                             Пр
                                                                                             Qγ
                                                                                                            qq
                                                                                                                                          qq
                                                                                                                                                                         Ωp
                                                                                                                            ŏ
                                                                                                                                                           οy
```

9;

Search completed: July 13, 2002, 10:53:18 Job time: 463 sec

us-09-733-756-2.rpr

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
```

- protein search, using sw model OM protein

Run on:

; Search time 42.58 Seconds
 (without alignments)
537.089 Million cell updates/sec July 13, 2002, 09:55:25

US-09-733-756-2 1301 Title: Perfect score:

.....REHLPLAVGIAFFLMTFLAS 238 1 MAAAPLLLLLLLVPVPLLPL.... Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283138 seqs, 96089334 residues 0.5 Searched:

283138 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* H 02 16 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SOMERIES	
	Score	Query Match	Length	ā	ID	Description
-	١	0.0	1 (4)	,	34	7 . 3 . 7
7	m	ω.	209	7	A54984	1 protein
m	43	ω,	Н	7	32	in-A2 - human
4	ω,	Ή.	C4	~	17	7 precursor
S	04.	1.	$^{\circ}$	~	80	sive axon
9	39	0	0	~	37	protein precu
7	•	æ	0	7	35	- human
ω	71.	₩,	$^{\circ}$	7	74	Coma
σ	71.	ω.	\sim	7	9	coma tr
10	48.		4	7	96	pd
11	43.	<u>.</u>	9	~	54	hetical prot
12	39.	ö	₹	~	8	ral/Epla2 p
13	32.	0	4	~	9	/ - r - s - r - c - c - c - c - c - c - c - c - c
14	\circ		356	~	36	heti
12	σ		20	_	2	e polyprote
16	88.5	•	\sim	7	7	-qalactosid
17	ω.		02	7	$\tilde{2}$	a-D-galactosi
8 ·	α		Η	7	33	thefical
9.0	85.5		70	7	7	tica
070	œ,		$^{\circ}$	7	7	tical
77	٠.		488	7	4	tical
22	82.5		S	7	25	yprote
23		•	9	-	TWFF	iption
24	82		3	~	1991	thetical prot
25	82		3	7	77	othetical p
<u>2</u> 6	85		~	7	8446	pothetical pro
27	82		2	7	883	obable transcr
58	ω		1144	7		etical pro
59	81.5			7	62	ockr2 - chicken

RESULT 2
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994

÷Ε	SNF2beta protein - alkaline phosphata	reversed polarity	0	probable protein w	a	hypothetical prote	transcription fact	chitinase (EC 3.2.	protein kinase C (genome polyprotein		thermopsin precurs
T19109 S39059	S45252 B72410	A54282 VCL,TMN	T01605	B84789	GBEC	T13389	138238	S05426	A32392	GNNY 4 P	S03822	н90370
22	7 7	7	7	7	1	~	7	~	7	~	~	7
457 1613	1647 434	612 859	202	498	1024	1291	321	328	700	2206	2206	570
6.2	6.2	6.1	6.0	6.0	0.9	0.9	0.9	0.9	0.9	0.9	6.0	0.9
81	81 79.5	79	78.5	78.5	78.5	78.5	78	78	78	78	78	77.5
30	33 33	34 35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SSULT 18849 18849 SRK-3 - P Species: Species: Accessic Kozlosky Cogene Title: I Referenc Accessic Status: Molecule Residues Cross-re Genetics	(man) quence_revision 29-May-1998 #text_change 29-Sep-1999 kovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S. 995 e receptor tyrosine kinases hek and elk: isolation of cDNAs e 849; MJID:95140419	<pre>translated from GB/EMBL/DDBJ L:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833 :438336; OMIM:601381 22 dance signal protein</pre>	tch 100.0%; Score 1301; DB 2; Length 238; 23 Similarity 100.0%; Pred. No. 1.7e-114; 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60 1+1+111111111111111111111111111111111	IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS 238
ESULT 38849 58849 58849 58849 5864058; 58621058	uman Homo sapiens (man) -May-1998 #sequence_ n: I38849 ', C.J.; Maraskovsky, 0, 299-306, 1995 igands for the recep e number: I38849; MU	ran: U1.	tch 100. 238; Conservative MAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLVPVPLLPLIMAAAPLLLLLLVPVPLLPLIMAAAPLLLLLLVPVPLLPLIMAAAPLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLVPVPLLPLIMAAAPLLLLLLLLVPVPLLPLIMAAAPLLLLLLLLVPVPLLPLIMAAAPLLLLLLLLLVPVPLLPLIMAAAPLLLLLLLLLVPVPLLPLIMAAAPLLLLLLLLLLLVPVPLLPLIMAAAPLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	IYCPHYNSSGVGPGAGPGPGF	LPQFTMGPNVKINVLEDFEGI
	RESULT 138849 LERK-3 - P C; Species: C; Date: 29 C; Accessic R; Kozlosky Oncogene 1 A; Title: I A; Referenc	A; Status: A; Status: A; Residues A; Cross-re C; Genetics A; Gene: G; A; Cross-re C; Genetics	Query Ma Best Loc Matches Qy 1	Oy 61 Db 61 Oy 121 Db 121	Qy 181 Db 181

S

17

Δ.

S

Tsai,

S.C.;

Yuan, J.Q.; Wong,

29-Sep-1999

#text_change

receptor involv

```
PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNAVDRPCLRLKVYVRPTNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC - NASQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQRYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VPEDKTERYVLYMVNFDGYSACDHTSKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                                                                                                                                                            a ligand for an Eph-related tyrosine kinase); MUID:95267434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GEN-POVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repulsive axon guidance signal protein RAGS precursor - chicken C; Species: Gallus gallus (chicken)
C; Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20.
C; Accession: A57084
R; Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, Cell 82, 359-370, 1995
A; Title: In vitro guidance of retinal ganglion cell axons by RAGS, A; Reference number: A57084; MUID:95360980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:91019430; PIDN:AAB60377.1;
                                                                                                                                                                                          N; Alternate names: AL-1
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_c]
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_c]
C; Accession: I58170; G01812
R; Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J. Neuron 14, 973-981, 1995
A; Title: Cloning of AL-1, a ligand for an Eph-related tyros A; Reference number: I58170; MUID:95267434
A; Reference number: I58170
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-228 <RES>
A; Roslosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P. Submitted to the EMBL Data Library, May 1995
A; Reference number: G08477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 415.5; DB 2;
Pred. No. 1.9e-31;
7; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VFDVNDKVE-NSLEPADDTVHESAEPSRGENAAQTPRI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary; translated from GB/EMBL/DDBJ
e type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMIM: 601535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: EPLG7; AF1; LERK7
A; Cross-references: GDB: 568757; OMINA; Map position: 13q33-13q33
C; Superfamily: axon guidance signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.9%;
larity 39.5%;
Conservative 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U26403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPOFTMGPNVKINVLEDFE-
                                                                                                                                                                                  irsor - human
names: AL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <K0Z>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
                                                     SHSGEKPVPT
                                                                                     LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-228 < A; Cross-references: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: G01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFFLMTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:
||LELLAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: m
                                                                                                                                                                                LERK-7 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDS
               117
                                                    171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status:
A;Molecule
                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A57084
                                                    á
                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δý
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding the huma
                                                                                                                                                                                _
                                                                                                                                                                           Cek7 receptor protein-tyrosine kinase
                for
              ligand
                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D:9368836
              xpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
                                                                                                                        3558837
ixit, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53
                                                                                                                                                                                                                                                                                       681887
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - EGYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                                                        PID:q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                      PIDN:AAA53636.1; PID:
M.F.; Siever, D.A.; D
                Ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ephrin-A2 - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
C; Accession: JE0322
R; Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A; Title: Cloning, chromosal mapping, and tissue expression of th
A; Reference number: JE0322; MUID:99045414
A; Accession: JE0322
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-213 <AAS>
A; Cross-references: GB:AJ007292; NID:93688367; PIDN:CAA07435.1;
C; Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                                                                                                              Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213;
           developmentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^{\rm ot}
                                                                                                                                                                                                                                                                                       PIDN: AAA68520.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                          33.6%; Score 437; DB 2; 1 larity 50.5%; Pred. No. 1.6e-33; Conservative 25; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 434; DB 2; Pred. No. 3.2e-33; 4; Mismatches 52;
A; Title: Identification and cloning of ELF-1, a A; Reference number: A54984; MUID:95007776
A; Accession: A54984
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-209 < CHE>
A; Cross-references: GB:U14941; NID:9558836; PIDN R; Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.
J. Biol. Chem. 270, 3467-3470, 1995
A; Title: cDNA cloning and characterization of a A; Reference number: A55873; MUID:95181289
A; Reference number: A55873
A; Reference number: GB:U14752; NID:9681886; PIDN A; Residues: 1-209 < SHA>
A; Residues: 1-209 < SHA>
A; Cross-references: GB:U14752; NID:9681886; PIDN C; Superfamily: axon guidance signal protein C; Keywords: lipoprotein; membrane protein
                                                                                                                                                                            Ø
               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.4%; Sc. Similarity 50.5%; Pr. 96; Conservative 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYEAPEPIFT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SINDYLDIYCPHY-
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SINDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

11;

Gaps

47;

Indels

228;

Length

99

125

117

180

173

--LLAI

--PSR---

PID:91019431

Σ.

Cerretti, D.P.; Carpenter,

pr

a 25 kDa tectal

J.; Noda, M.; Bonhoeffer,

20-Jun-2000

Tue

CDNAS

of

isolation

elk:

and

PID: 964283

3

13;

Indels

201;

Length

67

125

111

```
RESULT 8
184743
hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999
C;Accession: 184743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrc A;Reference number: 149766; MUID:95199254
A;Accession: 184743
A;Accession: 184743
A;Accession: 184743
A;Residues: 1-333 <RES>
A;Cross-references: GB:L38734; NID:9769675; PIDN:AAC41752.1; PID:9769676
C;Genetics:
A;Gene: GDB:EPLG5; LERK5
A;Cross-references: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33
                                                                                                                                                                                                                                                                                                                                                           8 LLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYN
                                                                                                                                                                                                                                                                                                                                                                                 --GPGPPEGPETFALYMVDWPGYESCQAEGPRAYKRWVCS---LPFGHVQFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                   SSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNAS - - QGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---WKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVLYMVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OADRCTIKKE-----NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNKDYYIIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNGSLEGLDNQEGGVCQTRAMKIL-MKVGQDASSAGSTRNKDPTRRPELEAGTNGRSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGYRTCNASQGFKRWECNRP----HAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN: AAC50079.1;
                                kinases hek
      Oncogene 10, 299-306, 1995
A; Title: Ligands for the receptor tyrosine kinases hek A; Reference number: 138849; MUID:95140419
A; Accession: 138850
A; Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-201 <RES>
A; Cross-references: EMBL:U14188; NID:9642834; PIDN:AAC C; Genetics:
A; Gene: GDB:EPLG4
A; Cross-references: GDB:438337; OMIM:601380
A; Map position: 1q21-1q22
C; Superfamily: axon guidance signal protein
                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDFEGENPQVPKLEKSI - - SGTSPKREHLPLAVGIAFFLMTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 171.5; DB 2
Pred. No. 2.3e-08;
3; Mismatches 100
                                                                                                                                                                                                                                                                                     Score 364.5; DB Pred. No. 9.9e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ-
                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 13.2%; So Similarity 28.3%; Professive 23;
                                                                                                                                                                                                                                                                                     28.0%;
44.5%;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 77; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 PTHNLH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:9179321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.; Lyman,
                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                     65
                                                                                D:9984118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                      linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8388.1;
                                                                                                                                                                                                                                                               LLLLLVPVPLLPLLAQGPG-GALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGGGAEQYVLYMVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYE
                                                                                                                                                                                                                                                                                  NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                         --VPEDKTERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPNGPLKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -POAHVNPOEKRLAADD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'eepe'
                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-
C; Accession: A36377
R; Holzman, L.B.; Marks, R.M.; Dixit, V.M.
Mol. Cell. Biol. 10, 5830-5838, 1990
A; Title: A novel immediate-early response gene of endothelium is in A; Reference number: A36377; MUID:91042512
A; Accession: A36377
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-205 <HOL>
A; Cross-references: GB:M57730; GB:M37476; NID:9179320; PIDN:AAA5838
C; Superfamily: axon guidance signal protein
                                                                                                                                                                                            ά;
A; Accession: A57084
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-228 <DRE>
A; Cross-references: GB: X90377; NID: g1061113; PIDN: CAA62027.1; PII
C; Superfamily: axon guidance signal protein
C; Keywords: glycoprotein; membrane protein; phosphatidylinositol
C; Keywords: glycoprotein; membrane protein; phosphatidylinositol
F; 1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                            22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: AAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 FHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      revision 29-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
E
                                                                                                                                                                                              Length
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.; McGrew, J.T.; VandenBos,
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76;
                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 2;
4.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                             FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV
                                                                                                                                                                                         404.5; DB
No. 2e-30;
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.0%; Score 390; DE larity 41.8%; Pred. No. 4.16 Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FKEGHSYYYISKPIHQHEDRCLRLKVTV-SGKITHS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225
                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEGENPOVPKLEKSISGTSPKREHLPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                      31.1%;
nilarity 49.1%;
Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I38850
LERK-4 - human
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_re
C; Accession: I38850
R; Kozlosky, C.J.; Maraskovsky, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
(man)
                                                                                                                                                                                                          Similarity 79; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
87; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                        EDS
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

N.; Matt

protein-tyrosine

7;

37;

Indels

333;

Length

149

---YEYYKVYMVDK

195

196

137

```
NVKINVLEDFEGENPQVPKLEKSISGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 YVLYMVSRNGYRTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 54
                                                                                                                  11
          189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                 g
           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                     Aspecies: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 14956
R; Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A; Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin A; Reference number: 149766; MUID:95199254
A; Reference number: 149766
A; Reference number: 149766; MUID:9769677; PIDN:AAC42052.1; PID:9769678
A; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -related tyrosine kina
                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Farrah,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYWNSSN-OHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYISTPTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WKCLRMKVFVCC---ASTSHSGEKPVPT-LPQFTMGPNVKINVLEDFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOADRCTIKKENTPLLNCAR - - - PDQDVKFTIKFQEFSPNLWGLEFQKNKDYYIISTSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 MVSRNGYRTCN-ASQGFKRWECNRPHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- STSHSGEKPVPTLPQFTMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
S46993
elk ligand - human
C; Species: Homo sapiens (man)
C; Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 28-May
C; Accession: 846993
R; Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.;
EMBO J. 13, 3757-3762, 1994
A; Title: Molecular characterization of a family of ligands for eph-rel
A; Reference number: 846993; MUID:94349923
A; Accession: 846993
A; Accession: 846993
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-346 < BEC>
A; Cross-references: GB:U09304; NID:9538366; PIDN:AAA53093.1; PID:95383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRPYEYYKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| :| : |: | | 137 TSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTTSRPSKEADNTVKMATQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| : | | : : | | : : | | : : | | : : | | SLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTNGRSSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 NRHAVYWNSSN-QHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---YEYYKVY
                                                                                                                                                                                                                                                                                                                                                                                                       Length 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 171.5; DB 2; llarity 28.3%; Pred. No. 2.4e-08; Conservative 27; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENPOVPKLEKSI -- SGTSPKREHLPLAVGIAFFLMTFL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%; Score 148.5; DB 2; 26.4%; Pred. No. 3.5e-06; ive 26; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKVDSKTVGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 KPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WKCLRMKVFVCCA--
RESULT 9
149766
hepatoma transmembrane kinase ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
62; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPTHNLH--
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CESP: F56A11
                                                                                                                                                                                                                           29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                           hypothetical protein F56All.3 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-
C; Accession: T32645
R; Gattung, S.; Goela, D.; Harper, M.
Submitted to the EMBL Data Library, December 1997
A; Reference number: 221204
A; Residues: 1-462 <GAT>
A; Residues: 1-462 <GAT>
A; Cross-references: EMBL: AF038619; PIDN: AAB92075.1; GSPDB: GN00022; CESIA; Experimental source: strain Bristol N2; clone F56All
C; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 4
A; Introns: 37/3; 69/2; 103/2; 220/1; 388/1; 412/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - - EY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 LIVYEVTEFAMDDCALESHSREVIRCAPEGTAEKVLRTQQLSGGRREDWKKOKVP--PKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- NASQGFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 FSEKFORYSAFSLGYEFHAGHEYYYISTPT-----HNLHWKC-----LRMKVFVCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 143.5; DB 2; Similarity 23.1%; Pred. No. 1.5e-05; 4; Conservative 30; Mismatches 93;
216
```

Accession: 148780
Stral/Eplg2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Species: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 148780; A55507; A55062; S52670
R;Boulllet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schubbur, B.; Doll Dev. Baol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryons A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryons A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryons A;Reference number: 148780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <-RES>
A;Cross-references: EMBL:248781; NID:g747858; PIDN:CAA88695.1; PID:g747859
A;Reletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene enc A;Reference number: A55507
A;Status: preliminary
A;Accession: A55507
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <-PLE>
A;Residues: 1-345 <-PLE> ۹. 2 enc embryona gene

Qy 162 KVFVCCASTSHSGEKPUPTLPOFTMGPNVKINVLEDFEGENPQVPKLEK 210	Query Match Reat Local Similarity 19.04; Pred, No. 0.13; Indeth 356; Reat Local Similarity 9.04; Pred, No. 0.13; Mismatches 64; Indels 84; Gaps 8; 64 35 VYMNSSNQHLREADTVOUNDYDLITCPHYSOVOPGAGEQOVULYNGSF 93 101 LYMNNSSYQHLREADTVOUNDYDLITCPHYSOVOPGAGEQOVULYNGSF 93 101 LYMNNSSYQHLREADTVOUNDYDLITCPHYSOVOPGAGEQOVULYNGSF 93 101 LYMNNSSYQHLREADTVOUNDYDLITCPHYSOVOPGAGEQOVULYNGSF 93 102 11 LYMNNSSYQHLREADTVOUNDYDLITCPHYSOVOPGAGEQOVULYNGSF 93 103 11 LYMNNSSYQHLREADTROUNDHHENGENEONERHARPSITESE
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M. J. Biol. Chem. 269, 26606-26609, 1994 A;Title: CDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyr A;Reference number: A55062; MUID:95014510 A;Rectaus: preliminary: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-89, Tr', 91-345 <sha> A;Cross.references: GB:U12983; NID:9575928; PIDN:AA53231.1; PID:9575929 C;Genetics: A;Genetics: A;Genetics</sha>	

```
6
                                                                                                                                                                                                                                                                                                                                                     CNASK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 PGGGAEQYVLYMVSRNGYRT----CNASQGFKRW-----ECNRPHAPHSPIKFSEKFQ 127
                                                                                                                                                                                                                                                                                                                                                                                                           --FHAGHEYYYISTPTHNLHWKCLRMKVFVCCAST 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VPKLEKSISGTSPKREHLP- 223
                                                                                                                                                                                                                     4; Gaps
                                                                                                                                                                                                                                                    26 GGALGNRHAV--YWNSSNQHLRREGYTVQVN-----VNDYLDIYCPHYNSSGVGPGAGPG 78
F;1028-1124/Product: core protein P2-5b #status predicted <P5B> .
F;1125-1453/Product: core protein P2-X #status predicted <P2X>
F;1454-1540/Product: protein P3-1b #status predicted <P1B>
F;1541-1562/Product: genome-linked protein VPg #status predicted <VPG>
F;1563-1745/Product: proteinase #status predicted <PTS>
F;1563-1745/Product: RNA-directed RNA polymerase #status predicted <RNS>
F;1746-2206/Product: phosphoryl-RNA (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                            21 GGSTINYTTINYYKDSASNAASKQDYSQDPSKFTEPLKDVLIKTAPALNSPNV--
                                                                                                                                                                                                                     9
                                                                                                                                                                               DB 1; Length 2206;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : : | : | TLDTVMWGKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQ---
                                                                                                                                                                                                                  109;
                                                                                                                                                                          Query Match
Best Local Similarity 20.5%; Pred. No. 8.1;
Matches 52; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LAVGIAF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::| ||
DYLLGCGVLIGNAF 259
                                                                                                                                                                                                                                                                                                                                                                                                          RYSAFSLGYE----
                                                                                                                                                                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                      ğ
                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
```

Search completed: July 13, 2002, 10:46:37 Job time: 3072 sec

i

.rai

-2

33-756

-7

```
MOLECULE TYPE:
S-08-240-124-2
2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

2000

                                                                                                                                                                                                    updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2, Appli
2, Appli
2, Appli
2, Appli
2, Appli
10, Appli
10, Appli
4, Appli
4, Appli
4, Appli
5, Appli
5, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g printed
                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ption.
                                                                                                                                                                                                                                                                                           FLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lave
                                                                                                                                                         Seconds
                                                                                                                                                  e 24.32 Second
t alignments)
Million cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d by chance to hathe result being re distribution.
                                                                                                                                                                                                                                                                                        REHLPLAVGIAFFLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Descr
                                                                                                                                                                                                                                                                                                                                                                                                                                                 231628
                                            Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pep.
                                                                                                                                                     rch time (without a 239.033 M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             results predicted be to the score of the total score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-240-124-2
US-08-453-943-2
US-09-057-121-2
US-09-358-734-2
US-09-358-734-2
US-08-455-001-2
US-08-455-001-2
US-08-455-001-2
US-08-920-440B-10
US-09-173-492-10
US-09-173-133-10
US-09-173-492-10
US-09-173-133-10
US-08-442-248-4
US-08-442-248-4
US-08-440-815-4
US-08-440-815-4
US-08-440-815-4
US-08-440-815-4
US-08-440-815-4
US-08-048-129-2
US-09-048-129-2
US-09-048-129-2
US-09-048-129-2
US-09-048-139-2
US-09-173-133-2
US-09-173-133-2
US-09-173-133-2
US-09-173-133-2
US-09-173-133-2
                                                                                                                                                       Search
                                                                                                                                                                                                                                                                                                                                                                                                                                            satisfying chosen parameters
                                                                                                                                                                                                                                                                                                                                                                                                      residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                     version
- 2000
                                                                                                            model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         summaries
                                                                                                                                                     :53:40
                                                                                                                                                                                                                                                                                                                                                         ι.
                                                                                                                                                                                                                                                                                    MAAAPLLLLLLLVPVPLLPL
                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                    24425594
                                                                                                            S.W
                    GenCore
(c) 1993
                                                                                                                                                                                                                                                                                                                                                         Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100%
45 St
                                                                                                                                                     60
                                                                                                            using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. is the number of r
greater than or equal
derived by analysis c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000000000
                                                                                                                                                     2002,
                                                                                                                                                                                                                                 US-09-733-756-
1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
Match
first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ユニス411451244151133445:24445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seds,
                                                                                                         protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238
238
238
238
238
209
209
209
220
2228
2228
2228
2228
1184
1184
1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                        Copyright
                                                                                                                                                                                                                                                                                                                                                        ٥.
                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.
                                                                                                                                                     13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maximum
Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
                                                                                                                                                                                                                                                                                                                                                                                                   31628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length:
length:
                                                                                                                                                     July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
10000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1000.0
1
                                                                                                                                                                                                                                                                                                                                                                                                                                             hits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126439
                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq
seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1301
1301
1301
1261
1261
1261
4437
4437
4415.5
4415.5
403
4403
4403
                                                                                                                                                                                                                                                                  core
                                                                                                                                                                                                                                                                                                                                  table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score gand is
                                                                                                                                                                                                                                                                                                                                                                                                                                             number
                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                   Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
                                                                                                                                                                                                                                         Title:
Perfect
                                                                                                                                                       on:
                                                                                                                                                                                                                                                                                                                                 Scoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               വര
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
No
                                                                                                                                                  Run
                                                                                                         Θ
```

```
      28
      403
      31.0
      184
      5
      PCT-US95-15781-2
      Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli 30.0
      205
      1
      US-08-448-736-1
      Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli 390
      30.0
      205
      1
      US-08-441-216-2
      Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli 390
      30.0
      205
      1
      US-08-299-567-4
      Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli 30.0
      205
      2
      US-08-445-065-1
      Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli 30.0
      205
      2
      US-08-959-524-1
      Sequence 1, Appli Sequence 1, Appli 364.5
      28.0
      179
      1
      US-08-959-524-1
      Sequence 1, Appli Sequence 1, Appli 364.5
      28.0
      179
      1
      US-08-959-524-1
      Sequence 1, Appli Sequence 2, Appli 364.5
      28.0
      179
      1
      US-08-959-524-1
      Sequence 1, Appli Sequence 3, Appli 364.5
      28.0
      179
      1
      US-08-959-511869-5
      Sequence 5, Appli 364.5
      28.0
      201
      1
      US-08-240-124-4
      Sequence 4, Appli 364.5
      28.0
      201
      1
      US-08-95-11869-5
      Sequence 4, Appli 364.5
      28.0
      201
      1
      US-08-95-11869-5
      Sequence 6, Appli 364.5
      28.0
      201
      1
      US-08-95-11869-5
      Sequence 7, Appli 364.5</
```

ALIGNMENTS

Tue

ö

.rai

~

56

-7 ϵ $\boldsymbol{\varsigma}$ -7

-09

```
120
                                                                                                                                                                     180
                                                                                                                                                                                              KPVPT 180
                                   Gaps
                                                           9
                                                                                      9
                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                   238
                                                    PHSPI
                                                                                                                PHSPI
                                                                                                                                                                                                                          LAS
                                                                                                                                                                                                                                                  AS
                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                        SURFACE
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.1a
    Score 1301; DB 1;
Pred. No. 2.7e-128;
                                                                                                                                                                                                                                                                                                                                                                                     THE CELL
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                      BECKMANN, M. P.
CERRETTI, DOUGLAS P.
VENTION: CYTOKINE THAT BINDS
VENTION: RECEPTOR HEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple System 7.1

SOFTWARE: Microsoft Word for Apple, V

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NIMER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                         51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08453943
Patent No. 5738844
                              ;
    100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BECKMANN, M.
APPLICANT: CERRETTI, DOU
TITLE OF INVENTION: CYTC
TITLE OF INVENTION: RECE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WASHINGTON
Query Match
Best Local Similarity
Matches 238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 51 UNI
CITY: SEATTLE
STATE: WASHING
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                    US-08-453-943-2
                                                                                                            61
                                                                                                                                      61
                                                                                                                                                                 121
                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                      RESULT
                                                                                  셤
                                                                                                                                     g
                                                                                                             ŏ
                                                                                                                                                                                          a
                                                        ò
                                                                                                                                                                 ŏ
                                                                                                                                                                                                                     δ
```

```
ö
                                                                                                                                                            120
                                                                                                                                                                                                            Gaps
                                                                                                         9
                                                                                                                                  9
                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                            238
                                                                                                                                                        MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                    181 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS
                                                                                                                                                                                                                                                                 LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS
                                                                              ö
                                                                              Indels
                                                 Score 1301; DB 1;
Pred. No. 2.7e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                             THE CELL
                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                                 red. No. 2. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     am 7.1
Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBER: US 08/114,426
30-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/161,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/057,121
                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09057121
Patent No. 5969110
GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT
TITLE OF INVENTION: RECEPTOR HER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: IMMUNEX CORPORATION 51 UNIVERSITY STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/240,124
                                       100.0%; Sc
100.0%; P?
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORM...
KATHRYN A.
72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-DEC-1993 RIOR APPLICATION NUMBER: US 06 FILING DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^{\circ}
                                                               Local Similarity 100 tes 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERISTICS
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS
ADDRESSEE: IMMUNEX C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: SEESE, KATHRYI
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: DATE STATE SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: SE
STATE: W
COUNTRY:
                                                                                                                                                                                                                                                                                                                                               US-09-057-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE C
LENGTH:
; MOLECULE
US-08-453-943
                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR
                                                                Best Loc
Matches
                                                                                                        Н
                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                181
                                                                                                                                                          61
                                                                                                                                                                                                                                       121
                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                        δ
                                                                                                                                 Q
Q
                                                                                                                                                                                   qq
                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                              ò
                                                                                                                                                          ò
                                                                                                                                                                                                                                                                 ô
```

amino acids

0;

Gaps

120

9

120

238

.rai

~

```
MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD
                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ;
                                                                                      238;
                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08299567
Patent No. 5747033
GENERAL INFORMATION:
APPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                     Score 1301; DB 4;
Pred. No. 2.7e-128;
                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               넊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l; DB 1;
4e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: Regeneron Pharmaceuticals, Inc
777 Old Saw Mill River Road
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1261;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/299,567 FILING DATE: 01-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REG
                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M.
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                    100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.9%;
illarity 97.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 amino acids
amino acid
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron F
STREET: 777 Old Saw Mi
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR SEQ ID
      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: pro
US-09-358-734-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                 Local Similarity
nes 238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity 233; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: ur
MOLECULE TYPE:
-08-299-567-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-299-567-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: INFORMATION F
                                                                                    Query Match
Best Local S
Matches 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local
Matches 2
                                                                                                                                                                                                                      61
                                                                                                                                           -
                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                   <del>Q</del>
                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                            g
                                                                                                                                          à
                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                     ò
                                                                                                              ö
                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                               180
                                                                                                              Gaps
                                                                                                                                 MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                                                                    238
                                                                                                                                                                                                                                                                                                                             238
                                                                                                                                                                                                     EKPVPT
                                                                                                                                                                                      IYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI
                                                                                                                                                                                                                                                                                                    FLAS
                                                                                                                                                                                                                                                                                                               FLAS
                                                                                                           ő
                                                                                  8
                                                                                                                                                                                                                                                                                             121 KFSEKFQRYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSG
                                                                                  23
                                                                                                                                                                                                                                            KFSEKFQRYSAFSLGYEFHAGHEYYY ISTPTHNLHWKCLRMKVFVCCASTSHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SURFACE
                                                                                    Length
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.1a
                                                                                Score 1301; DB 2;
Pred. No. 2.7e-128;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE CELL
                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version
                                                                                                                                                                                                                                                                                                                                                                  RESULI ...
US-09-358-734-2
; Sequence 2, Application US/09358734
; Patent No. 6274117
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, M. P.
; APPLICANT: CERRETTI, DOUGLAS P.
; TITLE OF INVENTION: CYTOKINE THAT BINDS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em 7.1
Apple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US 08/109,745
20-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/358,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MBER: US 08/114,426
30-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7
SOFTWARE: Microsoft Word for App.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/358,73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,172
ER: 2814-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/240,124
                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JNE: (206) 587-043
(: (206) 233-0644
756822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 amino acids
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 30-AUG-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-AUG-19
                             protein
  acid
                linear
                                                                                            11 Similarity 238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ
; TYPE: amino e
; TOPOLOGY: lir
; MOLECULE TYPE:
US-09-057-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                               Query Match
                                                                                            Local
                                                                                                                                                                                         61
                                                                                                        Matches
                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                            121
                                                                                            Best
                                                                                                                                                             q
                                                                                                                                                                                       ò
                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                    õ
                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                ò
```

ij

Gaps

g

```
||||||
|PHSPI 116
                                               IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI 120
                                                                                                   KPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SINDYLDIYCPHY-----GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                  238
                                                                                                                                                                          234
            NDYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AORPLEPILLE ----LEPERARNEDPARANADRYAVYWNRSNPRFQVSAVGDGGGYTVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                              22
                                                           MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNV
                                                                                                                                                                                                                                Sequence 2, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: Thereto
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAPLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 437; DB 1;
Pred. No. 5.4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : = = = = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d. No. 5.46
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 MAY 1995
N: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.6%;
ilarity 50.5%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE:
US-08-455-001-2
                                                                                                                                                                                                                                                                                                                                                                         Boston
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                     Σ
                                                                                                                                                                                                            SULT 6
-08-455-001-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Н
                                                                       61
                                                                                                                       117
                                                                                                                                                181
                                                                                                121
                                                                                                                                                                      177
                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
                                                                                                                                                                                                            RESULT
                        g
                                                                       Db
                                                                                                                       g
                                                 ò
                                                                                                 ŏ
                                                                                                                                                á
                                                                                                                                                                        g
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
17
113 PAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATPPNLVDRPCLRLKVYVRPTNET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SINDYLDIYCPHY-----GAPLPPAERMERYILYMVNGEGHASCDHRQRGFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 437; DB 4;
Pred. No. 5.4e-38
; Mismatches 4
                                                                                                                                  Sequence Sequence Sequence (Sequence ) Patent No. 62684/vo (SENERAL INFORMATION: APPLICANT: Flanagan, John G. APPLICANT: Cheng, Hwai-Jong (TITLE OF INVENTION: Thereto NUMBER OF SEQUENCES: 2 (CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(txt)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,814
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.709
R: HMI-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9511869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.6%; Scc
50.5%; Pre
+ive 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.5
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                              SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHSGEKPVPT 180
                                               : :|: |
173 LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|:
173 LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: 1
; MOLECULE TYPE:
US-08-308-814-2
                                                                                                                                                                                                                                                                                                                                                  02109
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
PCT-US95-11869-2
                                                                                                                      -08-308-814-2
                           171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                         RESULT
                                                          qq
                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
```

<u>,</u>

112

Gaps

18;

Indels

52;

Length 213

-EGYTVQV

170

176

```
---GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR
                                                                                                                                                                                            NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                     AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-
                              Score 437; DB 1;
Pred. No. 5.6e-38
1; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/08920440B
Patent No. 5919905
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2826-B
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Immunex Corporation: 51 University Street
Seattle
                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                   Cerretti, Douglas
FENTION: Cytokine
COUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                            33.6%;
ilarity 50.5%;
Conservative 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
FORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%;
| Similarity 50.5%;
| 96; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                     SINDYLDIYCPHY----
                                                                                                                                                                                                                                                                             LYEAPEPIFT 186
                                                                                                                                                                                                                                                  SHSGEKPVPT 180
                                             Similarity 96; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (2
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 51
CITY: Seat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98101
                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-920-440B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-08-920-440B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                           Best Local
                                                                                                                                                                   64
                                                                                                                                         54
                                                       Matches
                                                                                    ~
                                                                                                               4
                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                             177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                              d
                                                                                                                                                                   g
                                                                                                                                          ð
                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                              Related
                                                                                                                                                                                                                                                                                                                                                                                                 Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE-
                           EPH Receptor Ligands, and Uses
Thereto
                                                                                                                                                                                                                                                                                                                                                                                                               38;
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-609-324A-10

Sequence 10, Application US/09609324A

Patent No. RE37582

GENERAL INFORMATION:

TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6

FILE REFERENCE: A772

CURRENT APPLICATION NUMBER: US/09/609,324A

CURRENT FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 08/920,440

PRIOR FILING DATE: 1997-08-29

PRIOR FILING DATE: 1995-10-03

PRIOR FILING DATE: 1995-10-03

PRIOR FILING DATE: 1994-10-05
                                                                                                                                                                                                                                                                                                                                                                                               Score 437; DB 5;
Pred. No. 5.4e-38
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                        NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
                                                                                                                                               APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                             Floppy disk
4 PC compatible
FEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                          (617) 227-7400
(617) 227-5941
OR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 50.5%;
les 96; Conservative
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                   CURRENT APPLICATION DATA
                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                       TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                            IBM PC
                                                                                                        OPERATING SYSTEM: SOFTWARE:
                                                                                                                                                                                                                                                                                                                               inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : : : !
LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 1:
MOLECULE TYPE:
PCT-US95-11869-2
                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: LERU
US-09-609-324A-10
                                                                                            COMPUTER:
                                                                                                                                                                                                                                                          TELEFAX:
             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 10
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ga
```

```
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --EGYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR--
                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: System 7.6

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/920,440B
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 437; DB 2; I
Pred. No. 5.6e-38;
4; Mismatches 52;
P.
Designated LERK-6
                                                                                                                                                                              29-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
```

```
7;
-GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR 116
                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EGYTVQV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SINDYLDIYCPHY-----GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 437; DB 4;
Pred. No. 5.6e-38;
4; Mismatches 52;
                                                                                                                                                                                                                                APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                               ,--|
#
                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/320,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09/173,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2826-B
                                                                                                                                                                                      Sequence 10, Application US/09173492
Patent No. 6194172
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%;
nilarity 50.5%;
Conservative 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                    180
                                                                                                       : :|: |
177 LYEAPEPIFT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYEAPEPIFT 186
SINDYLDIYCPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 96; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                         Seattle
                                                                                    SHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: 1;
; MOLECULE TYPE:
US-09-173-492-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  98101
                                                                                                                                                            RESULT 11
US-09-173-492-10
                                                                                                                                                                                                                                                                                                                                       STATE: W
                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171
                           ò
                                                      В
                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINDYLDIYCPHY-----GAPLPPAERMEHYVLYMVNGEGHASCDHRQRGFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -EGYTVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AAAPLL-LLLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR---
                                                                                                                                                                                                                                                                                System 7.6
Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                   P.
Designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 437; DB 4;
Pred. No. 5.6e-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/920,440 FILING DATE: 29-AUG-1997 ATTORNEY/AGENT INFORMATION: NAME: Henry, Janis C. REGISTRATION NUMBER: 34,347
                                                                                                                                                                                                                                                                                                                         US/09/173,133
RESULT 12
US-09-173-133-10
; Sequence 10, Application US/09173133
; Patent No. 6232447
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
                                                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-B
                                                                                                                                         ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                              34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 287
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.6%; Sc.
larity 50.5%; Pr.
Conservative 24;
                                                                               APPLICANT: Cerretti, Douglas
TITLE OF INVENTION: Cytokine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flanagan, John G.
Cheng, Hwai-Jong
                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 amino acids
ino acid
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 96; Conser
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : :|: LYEAPEPIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-09-173-133-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino
                                                                                                                                                                                                                  98101
                                                                                                                                                                                         ž
                                                                                                                                                        STREET:
CITY: Se
STATE: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-455-001-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
```

Tue

5

.rai

```
Vincent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
                                                                                                                                                                                                                                                                                                                                                                         CPHYEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                T 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 173
                                                                                                                                                                                                                           Query Match
Best Local 3
                                                                                                                                     TYPE:
                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                    m
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                         П
                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                              φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CPHYEE-----PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 AAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAALLAAIVGVCV----WSDDPGKVISDRYAVYWNRSNPRFHRGDYTVEVSINDYLDIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|:
SPEPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPH Receptor Ligands, and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
    Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.4%; Score 421; DB 1; llarity 47.5%; Pred. No. 2.4e-36; Conservative 29; Mismatches 50;
    and
   Ligands,
                                                                                                                                                                                                                                                                                                                            HMI-011CP2
                                                                                                                                                                                                           31 MAY 1995
N: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION.

TITLE OF INVENTION.

NUMBER OF SEQUENCES: 5

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

AMDIUM TYPE: Floppy disk
                                                                                                                                                                                             -DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application PC/TUS9511869
GENERAL INFORMATION:
APPLICANT:
EPH Receptor
Thereto
                                                                                                                                                                                                                              APPLICATION: 800
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-(
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
           TITLE OF INVENTATIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
LAHIVE & COCKFIELD
                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                              Floppy disk
                                                         E: LAHIVE & COC 60 State Street
                                                                                                                                                                                                      SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 31 MAY 19
                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                 USA
                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 13
MOLECULE TYPE:
-08-455-001-4
                                                                                                                              02109
                                                                                                    Æ
          TITLE OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
PCT-US95-11869-4
                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                    --PLPAERMERYVLYMVNYEGHASCDHRQKGFKRWECNRPDSPSGPLK
                                                                                                                                                                                                                                                                                                                                                AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                   16;
                                                                                                                                                                                                                                                                             Length 200;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                              50;
                                                                                                                                                                                                                                                                       32.4%; Score 421; DB 5;
larity 47.5%; Pred. No. 2.4e-36
Conservative 29; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caras, Ingrid ...
Winslow, John W.
VENTION: AL-1 Neurotrophic Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             floppy disk
                            REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/442,248 FILING DATE: 15-MAY-1995 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb of the computer: IBM PC compatible operating system: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-442-248-4
; Sequence 4, Application US/08442248
; Patent No. 5759863
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
Matthew P. 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
                                                                                                                                                      200 amino acids
lino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Torchia, Timothy REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë
S
                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AL NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID N
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                          l Similarity
86; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                   amino
                                                                                                                                                                                  TOPOLOGY: 13

MOLECULE TYPE:

PCT-US95-11869-4
```

```
47; Gaps
                                                            Length 228
                                                                              Indels
                                                           Query Match
31.9%; Score 415.5; DB 1;
Best Local Similarity 39.5%; Pred. No. 1.1e-35;
Matches 98; Conservative 37; Mismatches 66;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 228 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-442-248-4
                                                                                                                                                                                                                                           ||: |
218 LLFLLAML 225
                                                                                                                                                                                                                                229 AFFLMTFL 236
                                                                                                              a
                                                                                                                                             qq
                                                                                                                                                                               g
                                                                                                                                                                                                               qq
                                                                                                                              Ω
                                                                                                                                                                                                                                                Dp
                                                                                                                                                               δ
                                                                                                                                                                                                ò
```

Search completed: July 13, 2002, 10:45:32 Job time: 3112 sec

.rag

~ ı

```
updates/sec
                                                                                                                       œ
                                                                                                                       23
                                                                                                                       FLAS
                                                            Seconds
                                                         Search time 57.73 Seco
(without alignments 457.917 Million cel
                                                                                                                      ..REHLPLAVGIAFFLMT
                                                                                                                                                                                         747574
4.5
Compugen Ltd
                                                                                                                                                                                        hits satisfying chosen parameters
                                                                                                                                                                     747574 seqs, 111073796 residues
 version - 2000
                                        mode]
                                                         2002, 09:49:45;
                                                                                                US-09-733-756-2
1301
1 MAAAPLLLLLLLLVPVPLLPL.
                                                                                                                                                  0.5
                                      protein search, using sw
GenCore
(c) 1993
                                                                                                                                                  Gapext
                                                                                                                                                                                                            0
2000000000
                                                                                                                                       BLOSUM62
Gapop 10.0
         Copyright
                                                          July 13,
                                                                                                                                                                                                           length:
length:
                                                                                                                                                                                        of
                                                                                                                                                                                                            sed
sed
                                                                                                                                       table
                                                                                                            score
                                                                                                                                                                                         number
                                                                                                                                                                                                         Minimum DB
Maximum DB
                                       OM protein
                                                                                                                    Sequence:
                                                                                                                                                                     Searched
                                                                                                Title:
Perfect
                                                                                                                                      Scoring
                                                          Run on:
                                                                                                                                                                                        Total
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*

6: /SIDS1/gcgdata/hold-geneseqy-embl/AA1986.DAT:*

7: /SIDS1/gcgdata/hold-geneseqy-embl/AA1986.DAT:*

8: /SIDS1/gcgdata/hold-geneseqy-embl/AA1988.DAT:*

9: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1989.DAT:*

10: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*

11: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*

12: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*

13: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*

14: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1991.DAT:*

15: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*

16: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*

17: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1996.DAT:*

18: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

19: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

20: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

21: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

22: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

23: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

24: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

25: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

27: /SIDS1/gcgdata/hold-geneseqy/geneseqp-embl/AA1999.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Description	Human hek-L protei	Mouse EPH receptor	Amino acid sequenc	Human LERK-6 polyp		Chicken EPH recept	Amino acid sequenc	Human AL-1, a liga	Lerk-7 protein. H	ot
SUMMARIES	AAR71481	AAR94766	AAW71006	AAY06822	ABG27837	AAR94767	AAW71007	AAR97854	AAW02586	AAW00035
DB	16.	17	19	20	22	17	19	17	17	17
Length DB	; 	209	209	213	335	200	200	228	228	228
% Query Match	100.0	. m	33.6	ω.	32.8	•	م	Ξ.	31.9	31.9
Score	30	43	$^{\circ}$	43	•	421	\sim	•	٠	415.5
Result No.	7	æ	4	ı,	9	Ž	ထ	σ	10	11

17 AAR91283 20 AAY06820 13 AAR23895 15 AAR3604 5 15 AAR82604 5 15 AAB54058 18 AAW18081 18 AAW18080 18 AAW18079 18 AAW18079 19 AAW18079 10 AAW18079 10 AAW18079 11 AAW18079 11 AAW18079 12 AAW18079 12 AAW18079 13 AAW18079 14 AAW18079 15 AAW18079 17 AAW106821 17 AAR91284 18 AAW33699 18 AAW33699 19 AAW46615 11 AAW33698 11 AAW33698 11 AAW33698 11 AAW06337 11 AAW06337 11 AAW06337 11 AAW06337 11 AAW06337	Lerk-6 protein. M LERK-6 protein. M Murine LERK-6 poly B61 protein sequen EBP. Homo sapiens Eph transmembrane eck receptor bindi Human PR0202 prote Human pancreatic c Truncated eck rece Human PR0202 polyp Human PR0202 polyp Human PR0202 protei LERK-6 exon polype Amino acid sequenc Human secreted pro EPH family ligand Human transmembran AL-2-short (AL-2s) Human cytokine Ler NLERK2 ligand for rece Ligand for recepto Full length ligand Ligand for recepto	
	90258 9128 9128 9128 9128 9128 9128 9128 912	
	7 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
	331.0 331.0 330.0 300.0	
	403 403 390 390 390 390 386 384 377.5 377.	
403 31. 403 31. 390 30. 390 30. 390 30. 386 29. 386 29. 387 29. 77.5 29. 77.5 29. 77.5 29. 179.5 29. 179 13. 179 13. 71.5 13.		

ALIGNMENTS

tyrosine kinase receptor; tumorigenesis; "signal peptide" Location/Qualifiers
1..19
/note= "signal peptic 238 Protein; entry) surface; (first protein standard; Ligand; cell Homo sapiens Human hek-L 03-OCT-1995 immunogen **AAR71481** AAR71481 Peptide Protein RESULT AAR71481 Kev

93US-0109745. 93US-0114426. 93US-0161132. 94US-0240124. 94WO-US09282 (IMMV) IMMUNEX CORP 20-AUG-1993; 30-AUG-1993; 03-DEC-1993; 09-MAY-1994; 17-AUG-1994; WO9506065-A 02-MAR-1995

Cerretti DP; Beckmann MP,

```
04-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR94766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  g
                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XX
XXX
XXX
XXX
XXX
XXX
FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                              pvpt 180
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                              The sequence is that of a novel protein designated hek-L, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis). It is also an immunogen for antibody production, as a reagent for detecting hek or hek-L in in vitro assays, to determine binding of hek proteins, to purify hek proteins, and to carry diagnostic or cytotoxic agents to particular leukaemia cells that express the hek antigen. Hek-L also binds the elk tyrosine kinase receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                                 238
                                                                                                                                                                                                                                                                                                                                                           PVPT
                                                                                                                                                                                                                                                                                                                                                                                               LPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLPLAVGIAFFLMTFLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family ligand;
                                        Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     regions
                                                                                                                                                                                                                                                                                                                                                        or its fusion product
therapeutic and
                                                                                                                                                                                                                                       238
                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ef1-2
                                       fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminal hydrophobic
                                                                                                                                                                                                                                      Score 1301; DB 16;
Pred. No. 8.1e-124;
Mismatches 0;
                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ef1-2; EHK1-L; Eph transmembrane tyrosine kinase neurological disorder; identification; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eph transmembrane tyrosine kinase family ligand,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "residue borders main
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPI-recognition tail
                                     New isolated DNA encoding hek-L protein useful as assay reagent or for carrying diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA
                                                                             36; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; Protein; 234
                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "carboxy
                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..235
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..30
/label=
218..235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
         WPI; 1995-106811/14
N-PSDB; AAQ85887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 238; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                              Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9527060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR82605;
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR82605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                             <del>, - i</del>
                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR8260.
```

g

Q

ο

ò

g

ò

ag

Ω

ò

```
Efl-2 (also known as EHK-1L) is an Eph transmembrane tyrosine kinase family ligand. It has homology with B61 (Efl-1) (see AAR82604). Efl-2 ends in a C-terminal hydrophobic sequence that appears to to be a recognition sequence allowing it to be GPI-linked and thus lacking in an intracellular domain. Efl-2 is useful for identifying other ligands for Ehk-1, -2, -3, Eck and Elk receptors. The ligands are useful in promoting a differential function and/or influencing the phenotye, such as growth and/or proliferation, of receptor bearing cells. They may be used in the diagnosis, and treatment of neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAAAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLD 60
                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFSEKFORYSAFSLGYEFHAGHEYYYISTPTHNLHWKCLRMKVFVCCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFKRWECNRPHAPHSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy
                                                                                                                                                           Maisonpierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tachycardia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1266; DB 16;
Pred. No. 2.8e-120;
); Mismatches 0;
                                                                                                                                                                                                                                                               nseq
                                                                                                                                                         Σ
                                                                                                                                                          Goldfarb
                                                                                                                                                                                                                                                              which bind Eph family receptors jical disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..20
/label= Sig_peptide
21..209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse EPH receptor ligand Elf-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                          ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor ligand; d
transgenic animal.
                                94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
                                                                                                                                                          Gale
95WO-US04208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.3%;
ilarity 98.3%;
Conservative
                                                                                                                         REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ...209
                                                                                                                                                         s,
                                                                                                                                                                                                           WPI; 1995-358635/46
N-PSDB; AAT03883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                         Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
234; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
                                                                                                                                                                                                                                                                                 neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                        Aldrich TH,
Yancopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elf-1; EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR94766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR94766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                       Aldrich
                                                                                                                                                                                                                                                                Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
```

.; H

60-sn

protein

of a mammalian Elf-1

sednence

Amino acid

(first entry)

20-0CT-1998

```
112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAS-T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel mouse EPH receptor ligand, Elf-1 (AAR94766), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15008) obtd. from an embryo mid- and hind-brain cDNA expression library. This cDNA is used for the rrodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                             diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sindyldiycphy----gaplppaermeryilymvngeghascdhrqrgfkrwecnr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54 NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYTVOV
                                                                                                                                                                                                                                                                                                                                       e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 209
                                                                                                                                                                                                                                                                                                                        Murine and chicken EPH receptor ligand, Elf-1 - useful in and treatment of disorders associated with the Elf-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                             site"
                                                                                                                   site"
                                                                       site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAPLLLLLLLVPVPLLPLLA - - QGPGGALGNRHAVYWNSSNQHLRRE-
                                                                     "potential N-glycosylation
                                                                                             N-glycosylation
                                                                                                                   N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.6%; Score 437; DB 17;
larity 50.5%; Pred. No. 3.6e-36;
Conservative 25; Mismatches 47;
                                               Core_sequence_motif
  Mat_protein
                         Cys4_motif
                                                                                          "potential
                                                                                                                 "potential
                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 86; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                 etc.
                                                                                                                                                                                                          95US-0393462
94US-0308814
                                                                                                                                                                                     95WO-US11869
/label=
69..159
/label=
                                35..166
/label=
                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                dementia, tachycardia,
                                                                     'note=
                                                                                            'note=
                                                                                                                  /note=
                                                                                                                                                                                                                                                                   Flanagan JG;
                           /lar
35.
                                                                                170
                                                                                                                                                                                                                                                                                      WPI; 1996-188446/19
N-PSDB; AAT15008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHSGEKPVPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | ||| ||||
agrpllpllll--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 lyeapepift
                                                        Modified-site
                                                                               Modified-site
                                                                                                     Modified-site
                                                                                                                                       WO9609384-A1
                                                                                                                                                              28-MAR-1996.
                                                                                                                                                                                                          27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                    19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                   Cheng H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ad
```

```
Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a mammalian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended itransplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid encoding Elf-1 protein that binds to EPH-type receptor for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                   site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 209;
                                                                                                                                                                                                                                          "potential N-linked glycosylation
                                                                                                                                                                                                                                                                                                                        "potential N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                  "potential N-linked glycosylation
                                                                                                                                                                                                                                       Score 437; DB 19;
Pred. No. 3.6e-36;
; Mismatches 47
                                                                                                                                                                                                                                                                                           "contains a Cys4 motif"
                                                                                                                                                                            /note= "signal peptide"
21..209
/note= "mature profess"
                                                                                                                                                      Location/Qualifiers
1..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0455001.
94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0455001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.6%;
ilarity 50.5%;
Conservative
                                                                                                                                                                                                                                                                              59..159
/note= "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flanagan JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-466665/40.
N-PSDB; AAV42926.
                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2A;
                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-1995;
19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fig
                                                                                                                                                                                                                                                                                                                                                                             US5795734-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local 9
                                                                                                                                                                           Peptide
                                                                                                                                                                                                     Protein
                                                                                                                                      Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                    Mus
                                                                                                                                                              Key
```

7;

Gaps

22;

Indels

25;

Local Similarity les 96; Conser

Matches

209 AA

Protein;

standard;

AAW71006

Π

AAW71006

RESULT

AAW71006

```
||||| : | | :|||||| | :
--llplrarnedparanadryavywnrsnprfqvsavgdgggytvev
    YTVQV
                                              NVNDYLDIYCPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNR
                                                                                           PHAPHSPIKFSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                       AAAPLLLLLLLVPVPLLPLLA--QGPGGALGNRHAVYWNSSNQHLRRE
                                                                                                                                          180
                                                                                                                                                               173 lyeapepift 182
             | ||| ||||
|agrp||p||1||--
                                                           sindyldiycphy
                                                                                                                                          SHSGEKPVPT
                     4
                                                                                            113
                                               54
                                                                      9
                                                                                                                  113
                                                                                                                                         171
                                                                    q
                                                                                           ογ
                                                                                                                  g
                                                                                                                                          ŏ
                                                                                                                                                               aa
```

standard; Protein; 213 AA (first entry) polypeptide. Human LERK-6 WO9910495-A1 Homo sapiens 24-JUN-1999 AAY06822 IJ RESULT AAY0682

injury; disease; LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity.

04-MAR-1999

98WO-US17772 27-AUG-1998;

97US-0920440 29-AUG-1997;

(IMMV) IMMUNEX CORP

Cerretti DP;

1999-243567/20 DB; AAX32767. N-PSDB;

New cytokine designated LERK-6

English. Claim 6; Page 42; 46pp;

comprising the LERK-6 nucleic acid sequences are used for the recombinant comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the chancement, stimulation, proliferation or growth of cells expressing the hek or elk receptor. The ligand and receptor complex may be involved in cheural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic of effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing theman LERK-6 polypeptide. The present sequence represents a

213 AA; Sequence

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical maging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations
                                       7;
                                         Gaps
                                                                   53
                                                                   --EGYTVQV
                                                                                                                                            sindyldiycphy----gaplppaermehyvlymvngeghascdhrqrgfkrwecnr
                                                                                 NVNDYLDIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASO-GFKRWECNR
                                                                                                                                                                                                     PHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; gene mapping; gene therapy; forensic; imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to assess
                                        18;
          Length 213;
                                        Indels
                                                                   AAAPLL-LLLLVPVPLLPLL-AQGPGGALGNRHAVYWNSSNQHLRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification or responsible for genetic disorders or other traits and
Score 437; DB 20;
Pred. No. 3.7e-36;
' Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 58196; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #27828
                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 335 AA.
                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
           33.6%;
50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping;
upplement; medical in
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                      Similarity 50.996; Conservative
                                                                                                                                                                                                                                               SHSGEKPVPT 180
                                                                                                                                                                                                                                                                           186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS92024
                                                                                                                                                                                                                                                                 : :|:|
lyeapepift
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                               ABG27837;
           Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                  ABG27837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                                                                                                     9
                        Best Loc
Matches
                                                                   ~
                                                                                                                                                         64
                                                                                                                                                                                      113
                                                                                                                                                                                                                                             171
                                                                                               4
                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                      ABG27837
                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                               ò
```

Tue

S

```
11;
    biodiversity
responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                     217
                                                                                                                                     Gaps
                                                                                                                                                                                                            ||:|:
phspng
                                                                                                                                                         NVNDYL
                                                                                                                                                                                                 PHAPHS
                                                                                                                                                                                                                                                 PIKFSEKFORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHS
                                                                                                                                                                                                                                                                                -GEN-POVPKLEKSISGTSPKREH
                                                                                                                                                                                                                                                                                                    -psr--
                                                                                                                                    47;
                                                                                                                 35;
                                                                                                                                                                                            DIYCPHYNSSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNR)
                                                                                                                                                                                                         MAAAPLLLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQV
                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tachycardia; therapy;
                                                                                                                  Length
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                               Score 426.5; DB 22
Pred. No. 7.8e-35;
; Mismatches 69;
                                                                                                                                                                   <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Core_sequence_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cys4_motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand Elf-1
                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                             GEKPVPTLPQFTMGPNVKINVLEDFE
                                                                                                                                   39;
                                                                                                             Query Match
Best Local Similarity 39.2%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor ligand; transgenic anima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0393462
94US-0308814
                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                          332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..21
/label=
22..200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22..200
/label=
61..150
/label=
33..157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33..157
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flanagan JG
                                                                                                                                                                                                                                                                                                                     LPLAVGIAFFLMTFL
                                                                                                                                                                                                                                                                                                                                 : | ||: |
---llaillfllaml
                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                  AA;
                                                                                                                                                                                                                 dvfcphyeds-
                                                                                 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9609384-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis;
                                                                                                                                                                                                                                                                                                278 hdr-
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                        AAR94767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cheng
                                                                                                                                                                                             09
                                                                                                                                                                                                                                      119
                                                                                                                                                                          106
                                                                                                                                                                                                                                                         218
                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                        321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Кеу
                                                                                                                                                                                                                                                                                                                                                                       SULT
                                                                                                                                                                                                                                                                                                                                                                                AAR947
αq
                                                                                                                                                                                                                 q
                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                             XX
DT
                                                                                                                                                      ð
                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   XX
PD
```

```
Chicken; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; cartilage; bone formation.
                                                                                                                                             involved in
                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
                                                                                                                                       A novel chicken EPH receptor ligand, Elf-1 (AAR94767), is involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It is the product of a cDNA clone (AAT15009) obtd. from an embryo cDNA expression library. This cDNA is used for the prodn. of recombinant Elf-1, which can be used to modulate proliferation, survival and/or differentiation of cells and tissues, and to stimulate or antagonise intracellular signal transduction
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                          diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                           CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIK
                                                                                                                                                                                                                                                                                                                                                                      AAPLLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGEKPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : || ::|||||| | ||||||||| ----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy
                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                              Length 200;
                                                      Ine and chicken EPH receptor ligand, Elf-1 - useful in treatment of disorders associated with the Elf-1 gene, antia, tachycardia, etc.
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence motif"
                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                               ; DB 17;
1.4e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
61..150
/note= "contains a Cys4 motif"
35..157
/note= "contains a core common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of an avian Elf-1 protein.
                                                                                                                                                                                                                                          pathways mediated by the EPH-type receptor.
                                                                                                                                                                                                                                                                                                                              d. No. 1.46
Mismatches
                                                                                                                                                                                                                                                                                                               32.4%; Score 421; 47.5%; Pred. No.
                                                                                                              Claim 1; Page 88-89; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 200 AA
                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0455001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                          Conservative
              WPI; 1996-188446/19
N-PSDB; AAT15009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                              aaallaaivgvcv-
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                     200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 cphyee----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5795734-A.
                                                                                                                                                                                                                                                                                                                                      86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                    dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus sp.
                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW71007;
                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW71007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW71007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \mathbf{p}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

9

```
228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFLMTFL 236
               Modified-site
                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: |
|1fllam1
                                                                         Binding-site
                                                                                                                                              WO9613518-A1
                                                                                                                                                                                                       07-JUN-1995;
27-OCT-1994;
                                                                                                                                                                                    26-OCT-1995;
                                                                                                                                                                09-MAY-1996
                                                                                                                                                                                                                                                       Caras IW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eds-
                                                                                                                                                                                                                                                                          WPI; 199
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                     for
                                                                                                                                                                          designated
                                                                                                                                                                  The present sequence represents an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended itransplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                         112
                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epif 172
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                            LDIY 62
                                                                                                                                                                                                                                                                                                                                                                                                         aaallaaivgvcv----wsddpgkvisdryavywnrsnprfhrgdytvevsindyldiy 60
                                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                   ISPIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPVP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -plpaermeryvlymvnyeghascdhrqkgfkrwecnrpdspsgplk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eph-related tyrosine kinase receptor; ligand;
'factor; neuropathy; angiogenesis; therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                          AAPLLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHLRREGYTVQVNVNDY
                                                                                                                                                                                                                                                                                                                                                                                                                                 CPHYNSSGVGPGAGPGGGAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSEKFORYSAFSLGYEFHAGHEYYYIS-TPTHNLHWKCLRMKVFVCCASTS-HSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for eph-related tyrosine kinase receptor
                                                                                                                                                                                                                                                                                                                                                      Length 200;
                                                                                                           Nucleic acid encoding Elf-1 protein that binds to EPH-type - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                    Score 421; DB 19;
Pred. No. 1.4e-34;
9; Mismatches 50;
                                                                                                                                                    53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 1..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                      29;
95US-0455001.
94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                    32.4%;
llarity 47.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                        HARVARD COLLEGE
                                                                                                                                                  75-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a ligand
                                                                               1998-466665/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                          Flanagan
                                                                                                                                                                                                                                                                                                                                                             Similarity
86; Conser
                                                                                                                                                                                                                                                                                                                        200 AA;
                                                                                                                                                   Claim 1; Columns
                                                                                         AAV42927
31-MAY-1995;
19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cphyee-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REK7
                                                                                                                                                                                                                                                                                                    formation
                                                           Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR97854;
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                            Query Mar.
-+ Local
                                                                                                                                                                                                                                                                                                                                                    Match
                                        (HARD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR97854
                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR97854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                            qq
                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     П
```

```
Human AL-1 (AAR97854) neurotrophic factor is a ligand for eph-related tyrosine kinase receptor REK7 (AAR97853). Its amino acid sequence was deduced from a cDNA clone (AAT18897) isolated from a human foetal brain cDNA library. Recombinant, mature AL-1 can be produced in transformed host cells. It may be useful in promoting the development, maintenance or regeneration of neurons in vivo, and can be utilised in methods for the diagnosis and/or treatment of neurological disorders. It can also be used to promote or enhance angiogenesis. Antagonists and agonists of AL-1, as well as antibodies raised against AL-1, also have therapeutic applns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --vpedkteryvlymvnfdgysacdhtskgfkrwecnrphspngplkfsek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSSGVGPGAGPGGGAEQYVLYMVSRNGYRTC-NASQGFKRWECNRPHAPHSPIKFSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- GEN-PQVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --llai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -psr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL-1 neurotrophic factor, an eph-tyrosine kinase ligand treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.
                                                              site"
                                                                                                                              site"
                                                                                                                                                                                             potential attachment site for glycophosphatidyl-inositol"
        / Jabel= Glycosylation
/label= Glycosylation
/note= "potential N-glycosylation si
162..164
/label= Glycosylation
/note= "potential N-glycosylation si
203..204
/label= GPI
/note= "potential attachment site fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 415.5; DB 17.
Pred. No. 6.1e-34;
7; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | || : -vfdvndkve-nslepaddtvhesaepsrgenaagtpri--
                                                                                                                                                                                                                                     214..228
/label= Hydrophobic_domain
Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0486449
94US-0330128
                                                                                                                                                                                                                                                                                                                                                                                          95WO-US14016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity 39.5%; 98; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPQFTMGPNVKINVLEDFE-
label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 54; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Winslow JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1996-239448/24.
)B; AAT18897.
```

11;

~

```
tein, usually
the N-terminus
9) was isolated
). The Lerk-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taches to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of human Lerk-7 protein. Lerk-7 is predicted to be anchored to the cell surface via glycosyl-phosphatidylinositol (GPI) linkage. A GPI anchor attaches to the exposed C-terminal amino acid of the processed mature protein, usually after cleavage upstream, often about 10-12 amino acids, of the N-termino of the hydrophobic domain. Lerk-7 coding sequence (AAT32699) was isolated using a probe derived from the murine Lerk-6 DNA (AAT32700). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                 residues"
                                                                                                                            culture; reagent;
  diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                face
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sur
to
                                                                                                                                                                                                                                                            1..133
/label= extracellular_receptor-binding_doma:
134..183
/label= spacer_region
194..208
                                                                                                                                                                                                                                                                                                                             of hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - which binds to cell
for delivering agents
                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                               stretch
                                                                                                                        hek; elk; cell surface receptor; disorder; injury; delivery agent; probe; cytokine.
                                                                                                                                                                                                                                       1..228
/label= precursor_protein
                                                                                                                                                                                                                                                                                                                                                      /label= GPI_attachment_
                                                                                                                                                                                              Location/Qualifiers
1..20
/label= signal_peptide
1..228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine
k, useful
                       AAW02586 standard; Protein; 228 AA
                                                                                                                                                                                                                                                                                                                            "C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37-38; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptors elk, hek and eck, u
for treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0396946
94US-0351025
                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US15781
                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human Lerk-7
                                                                                                                                                                                                                                                                                                                             'note=
                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1996-287171/29
DB; AAT32699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 AA;
                                                                                               Lerk-7 protein.
                                                                                                                                                probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                                                                                           WO9617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                    13-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                            05-DEC-1995;
                                                                        28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerretti DP;
                                                AAW02586;
                                                                                                                                     neuron;
Lerk-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                        Lerk-6;
                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 199
N-PSDB;
                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                Region
10
          AAW02586
```

```
Human HEK4 binding protein (HEK4 BP) (AAW00035) binds to and activates HEK4 and ECK receptors. Its amino acid sequence was deduced from a cDNA clone (AAT34292) isolated from a human placenta cDNA library. Expression vectors and host cells can be used for the prodn. of biologically active HEK BP. It is useful for modulating the growth and/or differentiation of EPH sub-family receptor-bearing cells, esp. in liver, kidney, lung, skin or neural tissues. It can be used to treat neural system disorders and in the regeneration of
                                                                         117
                                                                                                                            173
                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptors, partic. the HEK4 receptor - useful to differentiation of, e.g. liver and kidney cells, and nervous system disorders
LLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                              FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGEKPVPT
           --GEN-PQVPKLEKSISGTSPKREHLPLAVGI
                                                                                                                                                                             -----psr----1lai
                                                                                                                                                                                                                                                                                                                                                                                               HEK4 binding protein; HEK4 receptor; EPH-like receptor;
protein tyrosine kinase; ligand; growth; differentiation; cancer;
nervous system disorder; therapy; antibody.
                                                                                                              14 :: ||||:|| | ||:||||: | ||::||||| | |::|||||
fqlftpfslgfefrpgreyfyissaipdngrrsclklkvfvrptnscmktigvhdr-
                                                                                                                                                                  Ligand for EPH-like receptors, partic. modulate growth and differentiation of,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1..19
/label= Sig_peptide
20..228
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                              228
                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US01079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0379802
                                                                                                                                                   LPQFTMGPNVKINVLEDFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 39-40; 65pp;
                                                                                                                                                                                                                                                                                                                                                                      HEK4 binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fox GM;
                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996-362633/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to treat cancer
                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT34292
                                                                                                                                                                                                     AFFLMTFL
                                                                                                                                                                                                                       11: 1
218 llfllaml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9623000-A1.
                                                                                                                                                                                                                                                                                                                                                                                              HEK4 binding
                                                                          ----spa 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                             24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TD,
                                                                                                                                                                                                                                                                                                                     AAW00035;
                                                                                                                                                                                                                                                                                           AAW00035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bartley
                                                                                                                                                                                                                                                                   11
                                                                                                 126
                                                                                                                                                    181
                       9
                                                67
                                                                                                                          118
                                                                                                                                                                           174
                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI:
                                                                                                                                                                                                                                                                               AAW00035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                   RESULT
                       g
                                                                       Db
                                                                                                                          QQ
                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                    ò
                                                                                                   ò
                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
```

11;

Gaps

47;

Indels

8

Length

th 31.9%; Score 415.5; DB 17; Similarity 39.5%; Pred. No. 6.1e-34; 98; Conservative 37; Mismatches 66;

Query Match Best Local S Matches 98

```
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as
                                                                                                                                              180
                                                                                                                                                                                                                 173
                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a murine cytokine, Lerk-6, encoded by AAT32700. A fragment of murine Lerk-6 DNA was isolated by PCR for use a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see AAT32699). The Lerk-7 gene
                                                                                      Gaps
                                                                                                           99
                                                                                                                               65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                hek; elk; cell surface receptor; culture; reagent;
disorder; injury; delivery agent; diagnostic; therapeutic;
probe; cytokine.
                                                                                                       8 LLLLLLVPVPLLPLLAQGPGG-ALGNRHAVYWNSSNQHLRREGYTVQVNVNDYLDIYCPHY
                                                                                                                     :||||
fcphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface
to cells
                                                                                                                                                                                                                                                       -llai
                                                                                                                                                                                            KPVPT
                                                                                                                                                                                                                                    --GEN-PQVPKLEKSISGTSPKREHLPLAVGI
     cancer
                                                                8
                                                                                      1;
                                                                 22
                                                                                                                  FORYSAFSLGYEFHAGHEYYYISTP-THNLHWKCLRMKVFV----CCASTSHSGE
                                                                                                                                                                                                    Length
 tissues. Antagonists are useful for can also be used to raise antibodies.
                                                                                                                                                                                                                                                        ---psr-
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - which binds to cell
for delivering agents
                                                               DB 17;
                                                             Score 415.5; DB 17,
Pred. No. 6.1e-34;
37; Mismatches 66;
                                                                                                                                                                                                                                              | : |: | | | :
--vfdvndkve-nslepaddtvhesaepsrgenaaqtpri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lerk-7 cytokine
and eck, useful
disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49pp; English.
                                                                                  37;
                                                              31.9%;
illarity 39.5%;
Conservative 3
                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                 LPQFTMGPNVKINVLEDFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0396946
94US-0351025
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human Lerk-7 receptors elk, hek and ec)
 depleted
HEK4 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating neural
                                                                      1 Similarity
98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-287171/29
N-PSDB; AAT32700.
                               228 AA;
                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                             protein.
                                                                                                                                                                                                                                                                          AFFLMTFL
                                                                                                                                                                                                                                                                                       ||: |
|218 ||fllam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1995;
06-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9617925-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1996
damaged or treatment.
                                                             Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                               AAW02587
                                Sequence
                                                                                                                                                                                                                                                                                                                                                                    AAW02587
                                                                                                                                                                                                                                                                                                                                                                                                                                            neuron;
Lerk-7;
                                                                                                                                                                                                                                                                                                                                                                                                                               Lerk-6;
                                                                                                                                                                                                                                                                                                                                                                                                            Lerk-6
                                                                                                                                                                                         126
                                                                                                                                                                                                            118
                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                            RESULT 1
SXSS
                                                                                                                           g
                                                                                                       ŏ
                                                                                                                                                                    g
                                                                                                                                                                                         ò
                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                 òγ
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                             δ
```

```
and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                                                                                                                                                                                                140
                                                                                                                                                                                                                    115
                                                                                                                              Gaps
                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The LERK-6 polypeptide encoded can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by contact with the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to hek
                                                                                                                                                                                                                                                                                                                                                                                                             reagent;
ic: therapeutic
                                                                                                                                                  -GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG
                                                                                                                                                                                                       ---gaplppae
                                                                                                                                                                                            GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA
                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                which binds delivery and
                                                                                                       Length 184;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                             culture; read
                                                                                                                                                                                                                                          GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designated LERK-6 - useful for drug
                                                                                                    Score 403; DB 17;
Pred. No. 8.5e-33;
1; Mismatches 40
                                                                                                                                                                                                                                                    ell surface receptors; injury; delivery agent;
                                                                                                                                                                                                                                                                                                                     standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; 44pp; English.
                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening procedures.
                                                                                                                                                                                                                                                                                                                                                                                                             surface
                                                                                                   31.0%;
50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95WO-US12779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0538709
94US-0318393
                                                                                                                                                 ALGNRHAVYWNSSNOHLRRE-
                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-209575/21
N-PSDB; AAT14009.
                                                                     AA;
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           LERK-6; hek; elk; neurons; disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AA;
                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9610911-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-1995;
05-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP;
                                                                                                                                                                                                                                                                                                                                                                10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1996
                                                                                                                           82;
                                                                                                    Ouery Match
Best Local S
Matches 82
                                                                                                                                                                                                                                                                                                                                           AAR91283;
                                                                    Sequence
                                                                                                                                                                                                                                                                                                                    AAR91283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cerretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                      LERK-6
                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                           82
                                                                                                                                                                                                                                         141
                                                                                                                                                 28
                                                                                                                                                                      က
                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                          AAR91283
                                                                                                                                                                                                                                                                                               RESULT
SSSSSX
                                                                                                                                                                      g
                                                                                                                                                                                             δ
                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                              Оp
                                                                                                                                                                                                                                                                                                                                         XIXX
                                                                                                                                                                                                                                                                                                                                                                                                φ
                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                     ID
                                                                                                                                                                                                                                                                                                                                                                                     DE
```

S

. 4

S Н

16

Jul

5;

.rag

184 AA;

Sequence

```
Š
                                                                                                                                                                                                                                                                                                                                                                                    injury;
disease;
                                                                                                                  140
                                                                                                                        Gaps
                                                            81
                                                                                                           GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA
                                                         -GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG
                                                                                      -----gaplppae
                                16;
                                                                                                                                                                                                                                                                                                                                                                                alk receptor; human; murine;
neural tissue; neurological
   Length 184
                                                                                                                                                                   GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
                                                                                                                                                                                                  157
                                                                      Score 403; DB 17;
Pred. No. 8.5e-33;
24; Mismatches 40;
                                                                                                                                                                                e1k
                                                                                                                                                                                                                                                                                                                                                                             LERK-6 polypeptide; hek receptor; ecell proliferation; neural growth; neurodegenerative; excitotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46pp; English.
                                                                                                                                                                                                                                                                  standard; Protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US17772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0920440.
```

```
The B1 protein sequence was deduced from the cDNA sequence obtd. by screening a cDNA library from human umbilical vein endothelial cells with radiolabelled cDNA fragments derived from the 5' end of B61 DNA.

The B1 protein has 205 residues (24 kD) comprising a signal sequence and hydrophobic N- and C- terminal regions. The B61 gene is involved in early inflammatory response and serves as a marker. It may be detected by probes or by antibody-based immunoassay of biological fluids such as plasma, CSF or urine. These assays make it possible to predict a worsening in a disease process and allow the quantitative assessment of the magnitude of the inflammatory response. This information will allow the disease process and appropriate therapy, thereby shortening the disease process and limiting the patient's exposure to anti-inflammatory/immuno-suppressive therapy. B61 induction is rapid and profound, hence
                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                    induction;
                                                      -GYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGPGG
                                                                                                         GAEQYVLYMVSRNGYRTCNASQ-GFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHA
                                                                                 ---gaplppae
                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ρλ
  Length 184;
                                                                                                                                                                                                                                                                                                                                                                  therapy; in IL-2; TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        marker to detect inflammatory response
yene in biological fluids or by using
                              Indels
                                                                    GHEYYYIS-TPTHNLHWKCLRMKVFVCCAS-TSHSGEKPVPT 180
Score 403; DB 20;
Pred. No. 8.5e-33;
; Mismatches 40;
                                                                                                                                                                            Early inflammatory response; marker; antibody;
lipopolysaccharides; cytokines; Interleukin-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..18
/note= "signal pept.
                                                                                                                                                                                                                                                      AAR23895 standard; Protein; 205
                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
 31.0%;
ilarity 50.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91WO-US07704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0607741.
                                                      ALGNRHAVYWNSSNOHLRRE-
                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene prod. used as mark detecting the B61 gene hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                                                                                          sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Fig 3; 39pp;
                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1992-167172/20
B; AAQ24595.
             Similarity
82; Conser
                                                                                                                                                                                                                                                                                                                                                               inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-1990;
                                                                                                                                                                                                                                                                                                                                      B61 protein
                                                                                                                                                                                                                                                                                                            06-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9207094-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-1992
Query Match
Best Local S
Matches 82
                                                                                                                                                                                                                                                                                  AAR23895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XΜX
                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                  Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dixit
                                                      28
                                                                               m
                                                                                                         82
                                                                                                                                                               141
                                                                                                                                                                                                                             RESULT 1
                                                                              g
                                                                                                                                  g
                                                                                                                                                            ò
                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                  XXX
                                                                                                                                                                                                                                                                                                                                    DE
                                                                                                                                                                                                                                                                                                                                                                           XX
OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                  XX
FH
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PN
XX
PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTXX
```

```
9
                                                                                                                                                                                                                     24; Gaps
                                                                                                                                 it is easily detectable. The B61 response is highly specific proinflammatory stimuli, being only made by cells exposed to polysaccharides or cytokines such as IL-2 and TNF and not grofactors or interferon.
                                                                                         Length 205;
                                                                                                               Indels
                                                                                     Query Match
30.0%; Score 390; DB 13;
Best Local Similarity 41.8%; Pred. No. 2.1e-31;
Matches 87; Conservative 21; Mismatches 76;
                                                                                                                                                                                                                                                                198 FEGENPOVPKLEKSISGTSPKREHLPLA 225
                                                                                                                                                                                                                                                                            |:| | :| |
--pevrvlhsighsaaprl--fpla 191
                                                       205 AA;
                                                       Sequence
 ò
                                                                                                                                                       q
                                                                                                                                                                            ò
                                                                                                                                                                                                 qq
                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                            Ωp
                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                      qq
```

Search completed: July 13, 2002, 10:44:47 Job time: 3302 sec 33-756-1.rst

1-60-sn

```
Search time 1578.36 Seconds (without alignments) 14904.833 Million cell updates/sec
                                                                                                                                                                      1743
                                                                                                                                                                     aaaaa
                                                                                                                                                                    ....aaaaaaaaaaaaaa
                                                                                                                                                                                                                                                                  27472414
GenCore version 4.5
(c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                     13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                    US-09-733-756-1
1743
1 gctgctgctgctgctgc.....
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      using sw model
                                                                              2002, 08:40:20;
                                                                                                                                                                                                           Gapext 1.0
                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                                                                            IDENTITY_NUC Gapop 10.0,
                                                      nucleic search,
           Copyright
                                                                                July 13,
                                                                                                                                                                                                                                                                                             sed
                                                                                                                                                     score:
                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                         Minimum DB
Maximum DB
                                                   OM nucleic
                                                                                                                                    Title:
Perfect so
Sequence:
                                                                                                                                                                                                                                      Searched:
                                                                                 Run on:
```

em_estba:*
em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estro:*
em_htc:*
gb_est2:*
gb_htc:*
gb_htc:*
em_gss_hum:*
em_gss_inv:*
em_gss_linv:*
em_gss_linv:*
em_gss_linv:*

EST:*

Database

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution. Pred. N score g and is

	escrip	5095 ALS6509	533153 AL53315	563020	3747 602272	3158 6026343	8 AL572018	38 Mus mu	2 AL527972	37 6022691	0582	196 60270331	2 AL546822	30 60254	.57 CM3-NN	8904 xw97e11.	89015 xk98d10	786993 120664
SUMMARIES	3 ID	AL56509	AL533	AL56302	BF9697	BG7431	AL57201	AK0204	AL52797	BF96813	10 BF983120	BG69889	AL54682	BG4997	BF9531	BE138	AW18901	AW78699
	Length DB	80	030	86	13	02	20	85	84	26	804 1	62	02	47	96	20	ıo	35
op (Watch 1	0.	•	щ		6	ω.	ر. د	ъ.	2	33.2	2	;	0	5	ω,	۳.	ω.
	Score	•	72.	60.	18.	87.	25.	19.	15.	14.	78	26	•	30.	39°	16.	13.	0
÷	Nesur C No.	c 1	2	ლ ე	4		9 0	7	œ	o ;	10	T	12	Н ,	·	c 15	_	17

### ALTO STATE	c 18	400	 	.22	0 m v	\circ	10	78030 E6636	780303 holoh09. E663678 147613
17.6 20.0 84.4 10 875.2148 8 875.2148 600.6622148 600.6622148 600.6622148 600.6622148 600.6622148 600.6622148 600.6622149 600.6622149 600.6622140 600.662410 600.662	• (4 ()	י היי היי	5 0	-00	n 01	າທແ		1272654 RG70518	BE003141 120832 M 1272654 q159b04.x BG705182 60268810
15.0 15.0 25.2 9 ARG63808 ARG69808 ARG69809 ARG69808 ARG69808 ARG69808 ARG69809 ARG6980 ARG69809 ARG69800 ARG6980 ARG69809 ARG69800 ARG6980 AR	23	ייייי			100	3 44 (F54214	F542148 60206824
99.5 16.6 55.2 9 AAAC28407	25 25	n m	90		⊃ 4 •	~ co	5	669878	F977204 60214675 669878 113619 MA
76.4 15.8 298 9 BE048061 BE048001 L247412.7 26.9 15.4 523 10 BE64816 BE04816 ANJ23794 UI-W-BH2. 26.9 15.4 523 10 BE64816 BE04816 JOURN 1912.2 26.1 14.2 481 9 AA38749 ANJ23794 JOURN 1912.2 26.1 14.2 481 9 AA38749 ANJ23794 JOURN 1912.2 26.2 14.1 288 9 AA38749 ANJ23794 ENGAGOGO TO	26 27	000		9 9	90	വവ	0	28407 73105	628407 AL62840 I731050 603351
269 15.4 523 10 BEG4816 BEG48416 U.Y. FEE. 247 14.2 481 9 AA38813 AR200648 AR200648 AR200648 AA38813 AA388813 AA38813 AA388813 AA38813 AA38813 AA38813 AA38813 AA38813 AA38813 AA38813 AA38813 AA38813	N N	~	6. 27	N	8 ~	ᢐᢐ		4806 2379	048061 tz47d12 123794 HT-M-RH
46.2 14.2 48.9 5 AA28013 AA38813 AA38813 v.24400.7 46.2 14.1 288 9 AA38813 AA38813 AA38813 v.24400.7 46.2 14.1 288 9 AA38813 AA38813 AA38813 v.24400.7 46.2 14.1 288 10 B1753156 B175619 B175615 C03076012 F0308 13.2 775 10 T06133 F070619 B175615 UTR-R-L0-C02.2 12.7 354 10 B675619 B675619 UTR-R-L0-C03 E037619 UTR-R-R-L0-C03 E037619 UTR-R-R-R-R-R-R-R-R-R-R-R-R-R-R-R-R-R-R-	mr	C	26	М.	- ₹ 0	\sim	0	E64841	3648416 UI-M-BH
46.2 14.1 288 9 AA338749 AA338755 EXT9155 GO30205013 30.8 13.2 275 10 T04173 EXT9155 GO30205015 30.8 13.2 275 10 T04173 EXT9155 GO30205015 21.2 12.7 33.9 AA508818 BES55727 BES55727 ULR AA1-05020 EXT9153 GO30205015 21.2 12.7 33.9 AA508818 ASSE573 ULR AA1-05020 EXESTED TO BES55727 ULR AA1-05020 EXT9000 EXPS0520 ULR AA1-05020 EXPS0520 ULR AA1-05020 EXPS0520 ULR AA1-05020 EXPS0520 ULR AA1-05020 EXPS0530 ULR AA1-05020 EXPS0530 ULR AA1-05020 EXPS0530 ULR AA1-05020 ULR AA1-050	32	4	24	· ·	» α	ဝေ		38831	200648 daz4c06. 388313 vc24h03.
## 1. 78 10 BI73150 10 BI7350 10 BI7360 10 BI7	33	~ ~	٠ ن		· ~ ·	000		338749	338749 EST43752
21.2 12.7 354 10 86255727 B6555727 UTFRAIN 20 21.2 12.7 354 10 8625659 B6555727 UTFRAIN 21 21.2 7 354 10 8625659 B655659 B655659 B655659 B655659 UTFRAIN 21 21.2 7 354 10 8625659 B655659 B655659 UTFRAIN 21 21.2 7 354 10 8872090 B721090 B72	*) (*	70	. c	٠ •	C	$\sigma \sim$	00	175315	1753156 60302601 16173 FCT04062 F
21.2 12.7 354 10 B6376619 M506819 A150818 vc2403. 21.2 12.7 354 10 B6376619 M50818 vc2403. 21.2 12.7 332 9 A150818 A150818 A150818 vc240403. 91.2 12.6 258 10 B8725056 B721050 B5721050 B572105 B5721050 B721050	m	10			·	· C	0	F55572	555727 UI-R-A1-
10.2 12.6 238 10 m8950361	יי ריי	0 C	٠ م ۳	~ ~	~	ഥര	0	337661	3376619 UI-R-CU
19.8 12.5 970 10 BE721090 BE721090 BE721090 188082 MA 112.5 5750 9 AM199223 AM19923 AM199223 AM19923 AM199223 AM19923 AM	9 00	101	. 0	. ~	· w	10	0	F95036	7950361 CM3-NN11
17.4 12.5 700 9 AN199223 ASSESSED AN199923 CARACTOR AN19993 CARACTOR AN1990	40	(1)	ص ه	~ <	9 11	~ (0	E72109	E721090 188082 M
16.8 12.4 352 9 ANB63365 ANB63365 LA1612.x 15.6 12.4 364 9 AN980693 AN980693 AN9803653 UI-R-A1-d 206 11.8 324 10 BM386597 BM386597 UI-R-A1-d 206 11.8 324 10 BM386597 BM386597 UI-R-A1-d AL565095 LTI_ET015_Brn1 Homo sapiens CDNA clone CSODN003YL19 3 Prime, mRNA Sequence. AL565095 LTI_ET015_Brn1 Homo sapiens CDNA clone CSODN003YL19 3 AL565095 LTI_ET015_Brn1 Homo sapiens CDNA clone CONTA clone CONTACT. Genoscope CDNA clone CONTACT. Genoscope CDNA clone CONTACT. Genoscope CONTACT. France Familia CONTACT. Genoscope CONTACT. Genoscope CONTACT. Genoscope CONTACT. Genoscope CONTACT. Genoscope CONTACT. Genoscope CONTACT. France Familia CONTACT. Genoscope CONTACT. France Genoscope CONTACT. France Genoscope CONTACT. France Genoscope CONTACT. France CONT	4 4	N (V	٠.		n n	2 10	5	BF 24 UBU W199923	F240505 5018/5/2 199923 da24c06.x
AL565095 AL56095	4	~	9		*	10		186336	863365 tz47d12.
ALIGNMENTS ALIGNMENTS AL565095 AL565095 IT_FL015_Brn1 Homo sapiens CDNA clone Cs0DN003YL19 3 Prime, mRNA sequence. AL565095.1 GI:12916129 EST. AL565095.2 GI:12916129 EST. Homo sapiens ELMATYOTA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 1008) 1 (bases I to 1008) 1 (bases I to 1008) Contear: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 ERPX cedex - France Contearing Annualifiers 1 . 1008 Action/Qualifiers Action/Qualifiers Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL015_Brn1" Action=llb-LTI_FL016_Brn1" Action dinto the Not I and Eco RNA was digested with Not I and Cloned into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action into the Not I and Eco RNA was constructed by Life Technologies, a division of Invitry Action	44	0	20	∼: .:	4.0	10 01	0	A90105 BM3865	901053 UI-R-Al- M386597 UI-R-CN
AL555095 AL555095 LIT_FL015_Brn1 Homo sapiens CDNA clone CSODN003YL19 3 Prime, mRRA sequence. AL555095.1 GI:12916129 EST. AL555095.1 GI:12916129 EST. Homo sapiens Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Homo sapiens I.i.W.B., Gruber,C., Jessee,J. and Polayes,D. Li.W.B., Gruber,C., Jessee,J. and Polayes,D. Contact: Genoscope - Centre National de Sequencage BP 19 1006 EVRY cedex - France BP 19 19 1006 EVRY cedex - France BP 10 19 1006 - Contact: Genoscope - Centre Noul Infers Alexander - Contact - Metary was constructed by Life Technologies. Alexander - Metary was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Bmall : Highangelifetech.com URL : http://fullength.invitrogen.com" 209 a 262 c 325 g 175 primer - 17 others								ALIGNMENTS	
AL565095 LTI_ELD15_Brn1 Homo sapiens CDNA clone CSODN003YL19 3 AL565095 AL565095. Grant Homo sapiens CDNA clone CSODN003YL19 3 AL565095.1 GI:12916129 EST. human. Homo sapiens EVATYOURY LI,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization Unpublished (2001) Contact: Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@enoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers 1. 1008 Location/Qualifiers Location/Qualifie	RESULT AL5650								
prime, mRNA Sequence. AL565095 AL565095 AL565095 BST. human AL565095.1 GI:12916129 BST. human Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Homo sapiens Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope. Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Emali: seqreféquoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers 11008 //dranism="Homo sapiens" //db_xref="taxon:9606" //clone="CSODNO03YLL9" //clone="Taxon:9606" //db_xref="Taxon:9606" //clone="Taxon:9606" //clone="Taxon:9606" //clone="Taxon:9606" //db_xref="Taxon:9606" //db_xref="Taxon	LOCUS	. 2	ALS(000		FL01	Br	1008 bp mRNA 1 1 Homo sapiens cDNA cl	ear EST 16-FEB-200 e CSODN003YL19 3
AL265095.1 GI:12916129 EST. human. human. human. human. li (bases I to 1008) li (bases I to 1	0000		prin	0	l 03		o.		
buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Ammalia; Eutheria. Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 1008) Li, W.B., Gruber, C. Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr. Location/Qualifiers 1. 1008 //organism="Homo sapiens" //ob_xref="taxon:9606" //clone="toSoDNO03YL19" //clone="toSoDNO03YL19" //clone="toSoDNO03YL19" //clone="toSoDNO03YL19" //clone="toSoDNO03YL19" //clone="toSoDNO03YL19" //clone=lib="LTI_FL015_Brn1" //sex="male" //tissue_type="Adult brain" //sex="male" //tissue_type="Adult brain" //clone=lib="LTI_FL015_Brn1" //sex="male" //tissue_type="Adult brain" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //tissue_type="Adult brain" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //sex="male" //	VERSION		ALS(000	.1 G	I:12	161		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1008) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr. Location/Qualifiers 1. 1008 /organism="Homo sapiens" /db.ref="taxon:9606" /clone="CosbN003Y119" /clone="TosbN003Y119" /clone="TosbN003Y119" /clone="TosbN003Y119" /clone="TosbN003Y119" /clone="TosbN0003Y119" /clone="TosbN00003Y119" /clone="TosbN0003Y119"	KEYWORI	SO	EST.	_					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1008) Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Coneal: Movertor: Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan Library was communication of Invitrogen 9800 Medical Center Drive Rockville, Marylan flianglifetech.com URL: 100 a 262 c 325 g 195 t 17 others	ORGAN	MISM	НОШС	ар	ens				
<pre>1 (bases 1 to 1008) Liw.B., Gruber,C., Jessee,J. and Polayes,D. Liw.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Location/Qualifiers // Conneal incolongation // Contact incolonge Contact Incolongies of the pcMvSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL: http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others</pre>			Euka Mami	2 -	A; Me	azo eri	ÇΑ	ordata; Craniata; Ver imates; Catarrhini; H	ata; Euteleostomi idae; Homo.
Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Location/Qualifiers 11008 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="Tocation/Qualifiers /db_xref="taxon:9606" /clone="Lib="LTI_FL015_Brn1" /sex="male" /tissue_type="Adult brain" /tissue_type="Adult brain" /tissue_type="Adult brain" /tissue_type="Adult brain" /tissue_type="Adult brain" /tissue_type="Adult brain" /clone="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cD was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Lief Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax: (1) 301 610 8371 Email: fliang@ilifetech.com URL: http://tullength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others	REFEREI	NCE	, . , .	S.	3 1 t	0 10	_ '		•
Contact: Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - France Location/Qualifiers 11008 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="cS0DN003YL19" /clone="cS0DN003YL19" /clone="cS0DN003YL19" /clone="Libertype="Adult brain" /rissue_type="Adult	TITLE	E NAL	Full Unpu	. o .⊣	Grub yth c med (DNA DNA 2001	ibr	ssee,J. and Polayes,D ries and normalizatio	
<pre>BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr. Location/Qualifiers 11008</pre>	COMMEN	F	Cont	놨었	Geno ⊱ ເ	scopentr	Na	ional de S	
Location/Qualifiers Location/Qualifiers 1. 1008 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CSODN03YL19" /clone=lib="LTI_FL015_Brn1" /sex="male" /tissue_type="Adult brain" /tissue_type="Adult brai			BP 1		1006	EVRY	ced	x - France	, t
11008 /organism="Homo sapiens" /db_xref="taxon:9606" /clone=lib="LTI_FL015_Brn1" /sex="male" /tissue_type="Adult brain" /tissue_type="Adult brain" /note="Vector: pcMvSPORT 6; Site_1: Not1; 1st strand cD was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pcMvSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others	FEATURE			n	Loca	tion	Qua	ifiers	. 6113 .
/db_xref="taxon:9606" /clone="CS0DN003YL19" /clone_lib="LTI_FL015_Brn1" /sex="male" /tissue_type="Adult brain" /tissue_type="Adult brain" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cD was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others	S	Ŭ			_	100 ani	H =	sapien	
/clone_lib="LTI_FL015_Brn1" /sex="male" /tissue_type="Adult brain" /tissue_type="Adult brain" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cD was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others						ref e="	"ta SOD	a:9606" 03YL19"	
/tissue_type="Adult brain" /rissue_type="Adult brain" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cD was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others					/clo	e_1	_ q	I_FL015_Brn1	
/note="Vector: pcMvSPORT 6; Site_1: Not1; 1st strand cD was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pcMvSPORT vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others						ue.	уре	"Adult brain"	
enriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"					/not	 	cto d	<pre>: pCMVSPORT 6; Site_1: th a NotI-olido(dT) pr</pre>	NotI; 1st strand mer. Five orime e
cloned into the Not I and Eco RV sites of the pCMVSPORT vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"						ched	op .	e-stranded cDNA was	igested with Not I
Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Marylan 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 262 c 325 g 195 t 17 others					-	ed 1 or.	to	Not I and Eco RV S1 was constructed by	es of the pCMVSPORT ife Technologies.
10victogen 3800 medical center brive Nockville, marylan 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 others						act	. E.	Liang Life Technolog	es, a division of
fliang@lifetech.com URL : http://fulllength.invitrogen.com" 209 a 262 c 325 g 195 t 17 o					4 10	0, 0	# 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	x : (1) 301 610 8371	ROCKVIIIE, Maryian ail :
209 a 262 c 325 g 195 t 17 o					m C	ng@1 .//fi	fet	ch.com URL :	
	BASE CC	TNOC		Ø	111	262	777	325 g 195 t 17	thers

```
5;
                                                                                         1054
                                                                                                     1114
                                                                                                                 1174
                                                                                                                                                       1354
                                                                                                                                                                                             1534
             695
                                                                                                                                                                   1414
                                                                                                                                                                                1474
                                                                                                                                                                                                         1594
                                879
                                      815
                                                   874
                                                         760
                                                                      700
                                                                                  640
                                                                                               580
                                                                            994
                                                                                                                        460
                                                                                                                                    400
                                                                                                                                                340
                                                                                                                                                             280
                                                                                                                                                                          220
                                                                                                                                                                                      160
                                                                                                                                                                                                   100
                                                                                                                                                                                                                40
             cttgg
||||||
                                                   cgtag
||||||
CGTAG
                             GAGCA
                                      ggcta
                                                               ctctg
||||||
                          gagca
                                          GGCTA
                                                                                       tgttt
                                                                                                                        rgttī
                                                                                                                            ttca
                                                                                                                                                                       TTCA
                                                                                                                                                                              6;
 1008;
                          cttggaagg
|:|||||
|--TKGAAGG
                                                                                                                gggagcctttggcctctccaagggaagcctagtgggcctagacccctcctccatc
                                                  : | | |
|-|-|-
|: | | |
); DB 9;
.7e-109;
es 32;
                        Score 873.8;
Pred. No. 1.7e
4; Mismatches
                                                                                                                                                                                                                    14
50.1%;
ilarity 94.5%;
Conservative
   imilarity
   വ് പ
  Local
                               935
            9
                  991
                         Ø
                                     56
                                           878
                                                  816
                                                        9
                                                                    759
                                                                                 669
                                                                                              639
                                                                                                          579
                                                                                                                1115
                                                              S
                                                                           S
                                                                                                    ហ
                                                                                                                      519
                                                                                                                                   59
                                                                                                                                         235
                                                                                                                                               399
                                                                                                                             S
                                                                                                                                                            339
                                                                                                                                                                  355
                                                                                                                                                                               415
                                                                                                                                                                                     219
                                                                                                                                                                                           1475
                        69
                                                                                                                                                                                                        535
                                                                                                                                                                                                                    595
            63
                                                                                                                                                                                                              99
                                                                                                                                                                                                                          39
Query
Best I
                                                                                       99
                                                                                                    0.5
                                                                                                                             117
                                                                           93
                                                                                                                                   4
                               qq
                                           a
                                                                    g
                                                  ŏ
                                                        a
                                                                                              q
                                                                                 a
                                                                                                          d
                                                                                                                      d
                                                                           ò
                                                                                        à
                                                                                                    ò
                                                                                                                Q
                                                                                                                                   qq
                                                                                                                                         ò
                                                                                                                                               q
                                                                                                                             õ
                                                                                                                                                      õ
                                                                                                                                                           a
                                                                                                                                                                        a
                                                                                                                                                                                     d
                                                                                                                                                                  Q
                                                                                                                                                                                                              g
                                                                                                                                                                               ŏ
                                                                                                                                                                                           Q
                                                                                                                                                                                                 d
```

```
/tissue_type="Adult brain"
/tissue_type="Adult brain"
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
333 c 338 g 173 t 3 others
                               bp mRNA linear EST 13-FEB-2001 sapiens cDNA clone CS0DN003YL19 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
9
                                                                                                                                        Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gttccagcgctacagcgccttctctct-gggctacgagttccacgccggccacgagtact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1030;
                                                                                                                                       Vertebrata; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebr
Mammalia; Eutheria; Primates; Catarrhini; Homin
(bases 1 to 1030)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 872.6; DB 9;
Pred. No. 2.4e-109;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                1. .1030
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003YL19"
/clone_lib="LTI_FL015_Brn1"
/sex="male"
                             1030 bp
Homo sap
                         AL533153
AL533153 LTI_FL015_Brn1 H
prime, mRNA sequence.
AL533153
AL533153.1 GI:12796646
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.1%;
ilarity 97.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 945; Conser
                                                                                                             human
 7
                                        DEFINITION
                                                                                                                        ORGANISM
                                                                   ACCESSION
VERSION
                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
RESULT
AL533153
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
2001
                                                                                                                                                                                                                                                                                                                                                                        EB-:
                                                          538
                                                                         604
                                                                                         598
                                                                                                        664
                                                                                                                        658
                                                                                                                                                       718
                                                                                                                                                                                      778
                                                                                                                                                                                                                                                   868
                                                                                                                                                                      84
                                                                                                                                                                                                                    838
                                                                                                                                                                                                                                    904
                                                                                                                                                                                                                                                                   961
                                                                                                                                                                                                                                                                                   958
          48
                          47
                                                                                                                                                                                                                                                                                                                                                                       EST 16-FE
 SAGTACT
                                                         cagttc
||||||
                                                                                                                                                                                                                    atacat
||||||
                                                                                                                                                                                                                                                   gcacgg
:|||||
                       tctgctgcgcctccacatcgcactcc-ggggagaagccggtccccactctcccc
798 bp mRNA linear F
Homo sapiens cDNA clone CS0F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.genoscope.c
                                                                                                                                                                                                                                                 ctgtgtccgcccctctaccccttcccccacgtagggcactgtagtggaccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertonammalia; Eutheria; Primates; Catarrhini; Horata (bases 1 to 798)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="neuroblastoma cells"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _NBC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .798
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODC027YP19"
/clone_lib="LTI_NFL003_NE/Sex="male"
                                                                                                                                                                                                                                                                                                                                                                AL563020
AL563020 LTI_NFL003_NBC3 H
Prime, mRNA sequence.
AL563020
AL563020.1 GI:12912020
EST.
                                                                                                                                                                                                                                                                                                                               1021 GCCAAAA 1027
                                                                                                                                                                                                                                                                                                               965
                                                                                                                                                                                                                                                                                                                ggccaaa (
                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                     RESULT 3
AL563020/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
        425
                       420
                                       485
                                                       480
                                                                                                                                     665
                                                                                                                                                                                                                                  845
                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                      545
                                                                                      539
                                                                                                      605
                                                                                                                      599
                                                                                                                                                    629
                                                                                                                                                                    725
                                                                                                                                                                                    719
                                                                                                                                                                                                  785
                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                 839
                                                                                                                                                                                                                                                                905
                                                                                                                                                                                                                                                                                 899
                                                                                                                                                                                                                                                                                                962
                                                                                                                                                                                                                                                                                                               959
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                       qq
                                                                      d
                                                       ð
                                                                                                     g
                       õ
                                                                                                                     δ
                                                                                                                                                                    d
                                                                                      ð
                                                                                                                                    d
                                                                                                                                                    ð
                                                                                                                                                                                    ŏ
                                                                                                                                                                                                  d
                                                                                                                                                                                                                                 ga
                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                               à
```

```
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                 2;
                                                                                                                                                                                                                                                                         1104
                                                                                                                                                                                                                                                                                                    1164
                                                                                                                                                                                                                                                                                                                                                                                                                                             1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1524
                                                                                                                                                                                                                                                                                                                               1224
                                                                                                                                                                                                                                                                                                                                                            1284
                                                                                                                                                                                                                                                                                                                                                                                                                   1404
                                                                                                                                                                                                                                                                                      440
                                                                                                                                                                                                                                                           500
                                                                                                                                                                                                                                                                                                                 380
                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                                                                                                                                                                                         260
                                                                                                                                                                                                                                                                                                                                                                                                                                140
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                              aatgtacagacagagagtcccttccctcttaacccctgaccttcttgacttcccc
                                                                                                                                                                                                                                                                                                                                                                                                                                             cctcttttgtcttctgtgaagacaggacctatgcaacgcacagacattttggagaccg
                                                                                                                 3;
                                                                                                   79
                                                                                                    Length
                                                                                                                 Indels
                                                                                                   6.49
                                                                                                  Score 760.8; DB Pred. No. 3.7e-94; Mismatches
                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54
                                                                                                  Match 43.6%;
Local Similarity 97.9%;
es 782; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taaaacaacagcgcccct 1
                                                                       64
                                                                       BASE COUNT
ORIGIN
                                                                                                  Query Ma
Best Loc
Matches
                                                                                                                              745
                                                                                                                                            196
                                                                                                                                                          805
                                                                                                                                                                       738
                                                                                                                                                                                     865
                                                                                                                                                                                                   619
                                                                                                                                                                                                                925
                                                                                                                                                                                                                              619
                                                                                                                                                                                                                                            985
                                                                                                                                                                                                                                                          559
                                                                                                                                                                                                                                                                        1045
                                                                                                                                                                                                                                                                                      499
                                                                                                                                                                                                                                                                                                                                            379
                                                                                                                                                                                                                                                                                                                 439
                                                                                                                                                                                                                                                                                                                                                           1225
                                                                                                                                                                                                                                                                                                                                                                        319
                                                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                                                                                                                                                                                                                                                                                                                              1405
                                                                                                                                                                                                                                                                                                    1105
                                                                                                                                                                                                                                                                                                                               1165
                                                                                                                                                                                                                                                                                                                                                                                      285
                                                                                                                                                                                                                                                                                                                                                                                                                  345
                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                            g
                                                                                                                                                                       q
                                                                                                                                                                                                  q
                                                                                                                                                                                                                              ga
                                                                                                                                                          ò
                                                                                                                                                                                      ò
                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

Jul

Tue

```
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \mathbf{E}\mathbf{S}\mathbf{T}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                   360
                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNT
                                                                                                                                                                                                                                                                              540
                                                                                                                                                                                                                                                                                                                                                          009
1007
                                                                              1067
                                                                                                                                                          1127
                                                                                                                                                                                                                                        1187
                                                                                                                                                                                                                                                                                                                      1247
                                                                                                                                                                                                                                                                                                                                                                                                   1307
                                                                                                                                                                                                                                                                                                                                                                                                                                        629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG743158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE
                                                                             ò
                                       a
                                                                                                                 a
                                                                                                                                                             ŏ
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                     φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1013
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4360358"
/clone_lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/note="Organ: adrenal gland; 
                                                        ST 22-JAN-2001
4360358 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                   uteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                           on can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                                                                                                                                                                                                                                                                                                    (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1013)
1 (bases 1 to 1013)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10001 row: g column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 101
                                                       1013 bp mRNA linear E. Homo sapiens cDNA clone IMAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 718.8; DB 10;
Pred. No. 1.7e-88;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 715.
                                                                                                                                     GI:12336962
                                                                         NIH_MGC_84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.8%;
Matches 787; Conservative
                                                                                             mRNA sequence.
BF969747
BF969747.1 GI:
                                                      BF969747
602272160F1
                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ource
                マ
                                                                        DEFINITION
                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         887
                                                                                                                                VERSION
KEYWORDS
                               BF969747
                                                                                                                                                                                                                                                                                                                                     COMMENT
                RESULT
                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
```

```
linear EST 15-MAY-2001 cDNA clone IMAGE:4779506 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .702
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4779506"
/clone=lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.

SM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 702)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM10636 row: p column: 03

High quality sequence stop: 702.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dТ
                                                                           1126
                                                                                                                                                   1186
                                                                                                                                                                                                                               1246
                                                                                                                                                                                                                                                                                                        1306
                                                                                                                                                                                                                                                                                                                                                                                 1366
                                                                                                               479
                                                                                                                                                                                          539
                                                                                                                                                                                                                                                                  599
                                                                                                                                                                                                                                                                                                                                             658
                                                                                                                                                                                                                                                                                                                                                                                                                    718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG743158
602634316F1 NCI_CGAP_Skn3 Homo
mRNA sequence.
BG743158
BG743158.1 GI:14053811
```

0

Tu

ò

g

g

ò

d

õ

Op

g

δ

ō

a

õ

g

à

S

```
Query Match
                                                                                                                                                 Local
                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                   802
                                                                                                                                                                              750
                                                                                                                                                                                                     9
                                                                                                                                                                                                                            630
                                                                                                                                                                                                                                                   570
                                                                                                                                                                                                                 922
                                                                                                                                                                                                                                        981
                                                                                                                                                                                                                                                              1041
                                                                                                                                                                                                                                                                          511
                                                                                                                                                                                                                                                                                                 451
                                                                                                                                                                                                                                                                                                            1161
                                                                                                                                                                                                                                                                                      1101
                                                                                                                                                                                                                                                                                                                                                          1281
                                                                                                                                                                                                                                                                                                                        391
                                                                                                                                                                                                                                                                                                                                   221
                                                                                                                                                                                                                                                                                                                                              331
                                                                                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                  340
                                                                                                                                                                                                                                                                                                                                                                                             211
                                                                                                                                                                                                                                                                                                                                                                                                         1400
                                                                                                                                                                                                                                                                                                                                                                                                                                 1458
                                                                                                                                                                              ga
                                                                                                                                                                                          ò
                                                                                                                                                                                                    D
                                                                                                                                                                                                                            g
                                                                                                                                                                   ŏ
                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                              ST 16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                            uteleostomi;
                                                                                                                                                                                                           1034
                                                                                                                                                                                                                                 1094
                                                                                                                                                                                                                                                        1154
                                                                                                                         240
                                                                 674
                                                                                                              794
                                                                                                                                                300
                                                                                                                                                                        360
                                                                                                                                                                                               420
                                                                                                                                                                                                                                            540
                                                                                                                                                                                                                                                                   900
                                                                                                                                                                                                                                                                                          629
                              Gaps
                                                     9
                                      tttgtc
|||||||
                                                              agagcatcagcgggaccagccccaaacgggaacacctgccctggccgtgggcatcgcct
                                                                                                            cccatt
||||||
                                                                                                                                                                                                                                                        ctgcct
||||||||||
||CTGCCT
                                                                                     1;
                   02
                                                                                                                                                                                                                                linear E
                                                                                                                                                                                                        gctcaggactccctggcccctggtacctttccctgactcctggtgccctctccci
                                                                                                                                                                                                                                                      -- O
                                                                                                                                                                                                                                                                                                                                                                                            Vertebrata;
i; Hominidae
                              Indels
                                                                                                                                                                                                                                                                                                                702
                                                                                                                                                                                                                                                                                                                                                                                                             and Polayes, D. normalization
                  10
                            2;
                                                                                                                                                                                                                                                                                                    bp mRNA
sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                            Craniata; V.
Catarrhini;
                  DΒ
                       84;
                 ore 687.8;
ed. No. 3e-8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              ā
                                                                                                                                                                                                                                                                                                                                                                                                             J. and
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 750)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and Unpublished (2001)
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                             750
Homo
                 Score
                                                                                                                                                                                                                                                                                                                                           AL572018
AL572018 LTI_NFL006_PL2 H
Prime, mRNA sequence.
AL572018
AL572018.1 GI:12929883
EST.
                            ó
                Match 39.5%
Local Similarity 99.6%
es 700; Conservative
                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                RESULT 6
AL572018/c
LOCUS
                Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                        55
                                                                                                            735
                                                                                                                                                                                                                                                                                                                                                                                     S_{\overline{\mathbf{M}}}
                                                                          61
                                                              S
                                                                                      S
                                                                                                 121
                                                                                                                       181
                                                                                                                                                                      301
                                                                                                                                                                                 915
                                                                                                                                                                                                       975
                                                                                                                                                                                                                                           481
                                                                                                                                   S
                                                                                                                                                          55
                                                                                                                                                                                             361
                                                                                                                                                                                                                   421
                                                                                                                                                                                                                               035
                                                                                                                                                                                                                                                                             1155
                                                                                                                                                                                                                                                                                                               099
                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                      1095
                                                                                                                                                                                                                                                                  541
                                                                                                                                                                                                                                                                                        601
                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                               61
                                                                                      67
                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                    ORGANI
                                                                                                                                                          æ
ORIGIN
```

g

ò

q

ò

a

g

õ

q

õ

ò

```
7;
                                                                                                                                                                                                1040
                                                                                                                                                                                                                   1100
                                                                                                                                                                                                                                     1160
                                                                                                                                                                                                                                                                           1280
                                                                                                                                                                                                                                                                                                                  1399
                                                                                                                                                                   631
                                                                                                                                                                                                                                                                 332
                                                                                                                                                                                                                                                                                     272
                                                                                                                                                                                                                                                                                                                           152
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                      tecteccatggetagaagtggggeetgeaccatacatetgtgteegeeeeetetaleeeetetaleeeetetaleeeetetaleeeeetetaleeeeetetaleeeeete
                                                                                                                                                         ggatgccaaggggtgggcattggggtgccaggcatgtacagactctatatct-cta
                                                                                                                                                                                                                                                                                                                 ccctggcccctctttgtct---tctgtgaagacaggaccta-tgcaacgcacagacact
                                                                                                                             6
                                                                                                                   750
                                                                                                                    Length
                                                                                                                             Indels
                                                                                                                   Score 625.4; DB 9;
Pred. No. 8.4e-76;
; Mismatches 18;
                                                                                                                             16;
                                                                                                                   ch 35.9%; Similarity 94.3%; 706; Conservative
```

```
1 Similarity
905; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ದ್ದ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S dases 1 to 1085)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                          diaphragm region
                                                                                                                                                                                                                      HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                       embryonic body
A, clone_lib:RIKEN:9430025D14.
                         32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Team and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute
for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ection
co11
                                                                                                                                                                                                                                                                                                                                                             Mus musculus (strain:C57BL/6J) 12 days embryo embryons
between diaphragm region and neck cDNA to mRNA, clone
full-length enriched mouse cDNA library clone:9430025
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                            AK020438
Mus musculus 12 days embryo embryonic body between and neck cDNA, RIKEN full-length enriched library, clone:9430025D14:ephrin A3, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. Hayashizaki, Y. Direct Submission Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Exploration Research Group Phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a full-length mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (sites)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                          \boldsymbol{\varepsilon}
                                                            4 (sites)
The RIKEN Genome Exploration
FANTOM Consortium.
Functional annotation of a f
Nature 409, 685-690 (2001)
5 (bases 1 to 1085)
                                                                                                                                                                                                                                                                                                                           GI:12861020
                                                                                                                                                                                                                                                                                                                                           HTC; CAP trapper
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                  AK020438
AK020438.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11076861
                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
                                                            1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                    RESULT
AK020438
                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                             Qγ
                                                                                                     qq
```

```
/clone_lib="RIKEN full-length enriched mouse cDNA library"/dev_stage="12 days embryo"
  (GSC),
Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=3
/protein_id="BAB32100.1"
/db_xref="GI:12861021"
/translation="DFEGENPOVPKLEKSISGTSPKREHLPLAVGIAFFLMTLLAS'
1066. .1071
                                                       Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Exploration Research Group, RIKEN Gemomic Sciences Center (CRIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aagactttgagggagaaccctcaggtgcccaagcttgagaagagcatcagcgggacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGACTTTGAGGGAGAATCCCCAGGTGCCCAAGCTTGAGAAGAGCATCAGTGGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                     source key: MGI: 106644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 619.6; DB 11;
Pred. No. 4.6e-75;
; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                /note="data source:MGD,
evidence:ISS
ephrin A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative"
334 c 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="putative"
1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                  /gene="Efna3"
                                                                                                                                                                                                                                                                                                                                                                                                        'gene="Efna3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
ilarity 80.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179
```

Ø

ns

```
1046
                                              1106
                                                         1166
                                                                     1226
                                                                                1286
                                                                                            1346
                                                                                                       1406
                                                                                                                   1466
                                                                                                                              1526
                                                                                                                                                     1646
      279
                       986
                             397
                                                                                                 743
                                        457
                                                               571
                                                                           631
                                                                                      683
                                                                                                             803
                                                                                                                         859
                                                                                                                                    918
                                                                                                                                          158
                                                                                                                                               977
                                                                                                                                                           103
               III II
GCC-TG
                                                                    ggttt
            gccttg
                                 accgta
|||||
ACCGT-
 ttcccc
      CACTCT
                      -cccrc
                                                                       GGTTT
                                                                                     --TGG
                                                                                           11111
11111
100000
                                                                                gatge
                                                                                                      ccttc
                                                                                                                                                    cctgtttacagcaataagcacgtcctcctccccactcccacttccaggattgt
                                                                               œ
     20
813
           867
                280
                      927
                            339
                                       398
                                             047
                                                  458
                                                                    1167
                                  987
                                                              Ŋ
                                                                          572
                                                                                                            744
                                                        1107
                                                                                     632
                                                                                           1287
                                                                                                 684
                                                                                                                                   860
                                                                                                                                                                     1036
                                                                               1227
                                                                                                       1347
                                                                                                                  1407
                                                                                                                        804
                                                                                                                              467
                                                                                                                                         527
                                                                                                                                              919
                                                                                                                                                    587
                                                                                                                                                          978
                                                                                                                                                                647
                                                              51
     셤
                qq
                                       d
                                                  q
                                                              d
           ð
                      ò
                            d
                                  Q
                                                        Ω
                                                                          d
                                                                                     g
                                                                                                 d
                                                                                                            pp
                                             Qγ
                                                                    ò
                                                                                                                                   a
                                                                               δ
                                                                                           δ
                                                                                                       à
                                                                                                                  ò
                                                                                                                        g
                                                                                                                                              d
                                                                                                                                                          a
                                                                                                                              ò
                                                                                                                                                    ð
                                                                                                                                         ò
                                                                                                                                                                     q
```

```
: EST 13-FE3-2001
CS0DC027YP19 5
                                                                                                   Œ
                                                                                                  Vertebrata; ; Hominidae;
                       linear
clone (
                      l bp mrwn
no sapiens cDNA
                                                                                                  Craniata; Ve
Catarrhini;
                     684 b
Homo
                                                                                                Chordata;
Primates;
                               m
                                NBC
                                                            9
                  AL527972
AL527972 LTI_NFL003_NI
prime, mRNA sequence.
AL527972
AL527972.1 GI:127914(
EST.
                                                          GI:127914
                                                                           human.
Homo sapiens
Eukaryota; Metazoa; (
Mammalia; Eutheria; 1
                            DEFINITION
                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                    ORGANIS
RESULT
AL527972
LOCUS
```

```
1. .684
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODC027YP19"
/clone=lib="LTI_NFL003_NBC3"
/fissue_type="neuroblastoma cells"
/tissue_type="neuroblastoma cells"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Library was constructed by Life Technologies. Contact: Feng Library was haryland 20850, USA Fax: (1) 301 610
8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
http://fulllength.invitrogen.com"
                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                          Center
610
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                            : www.genoscope.cns
                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                  684;
                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                         Indels
l (bases 1 to 684)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.gen
                                                       pe - Centre National de Sequencage
91006 EVRY cedex - France
seqref@genoscope.cns.fr, Web : www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Score 615.6; DB 9;
Pred. No. 1.8e-74;
; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                        35.3%; Sc.
89.3%; Pre
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                             l Similarity
609; Conser
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 609
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                  ч
                                                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       556
                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

Db 181 AGACATATGCCCC Qy 1104 caggggcagaaca	gattga 		7 99 6 CA 7 tt 1 1 0 TJ	ACCESSION BF983120 VERSION BF983120.1 KEYWORDS EST. SOURCE human. ORGANISM HOMO Sapiens Eukaryota; 1 Mammalia; E1 REFERENCE 1 (bases 1 AUTHORS NIH-MGC http://orginalisebed	Contact Email: Tissue CDNA L CDNA L CDNA E DNA Se Clone found t http:// Plate: High qu
541 GAAGATMAACGTGCTGGAAGACTTTGAGGGAGAACCCTCAGGTGCCCCAAGCTTGAGAA 600 616 gagcatcagcgggaccagaccaaacgggaacacctgccctggccgtgggcatcgcctt 675	BF968137 MRNA sequence. BF968137 BF968137.1 GI:12 EST. human. Homo sapiens Eukaryota; Metazo Mammalia; Eutheri	1 (bases 1 to 826) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collec Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc.	found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9993 row: p column: 06 High quality sequence stop: 769. Location/Qualifiers 1826 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4357493" /clone=lib="NIH_MGC_84" /tissue_type="adrenal cortex carcinoma, cell line" /tissue_type="adrenal cortex carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_Noti; Site_2: Sall; Cloned unidirectionally; oligo-dr	Match Social Similarity 89.4%; Pred. No. 2.5e-74; Social Similarity Social Social Social Similarity Social Similarity Social Social Social	64 ccccacgtagggcactgtagtggaccaagcacgggacagccatgggtcccgggcggc 923 [1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 54 Qy 61 Db 60 Qy 67 Db 66 Db 66		REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	SE CO IGIN Query Best Match	Oy 86 Oy 92 Oy 98 Oy 98 Oy 98 Oy 104

```
804 bp mRNA linear EST 23-JAN-2001
Homo sapiens cDNA clone IMAGE:4397263 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://mgc.nci.nih.gov/.

I Institutes of Health, Mammalian Gene Collection (MGC) shed (1999)

: Robert Strausberg, Ph.D.

: Robert Strausberg, Ph.D.

: Gapbs-r@mail.nih.gov

Procurement: ATCC

ibrary Preparation: Life Technologies, Inc.

ibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)

quencing by: Incyte Genomics, Inc.

distribution: MGC clone distribution information can be hrough the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov

LLAM10097 row: 1 column: 08
                        1163
                                                                                                                     1283
                                                                                                                                                                                                                   1403
                                                                                                                                                                                                                                                                  1461
                                                                                                                                                                                                                                                                                                               1516
                                                                                                                                                                                                                                                                                                                                                           1576
                                                                                                                                                                                                                                                                                                                                                                                                           1636
                                               300
                                                                                              360
                                                                                                                                             420
                                                                                                                                                                                            480
                                                                                                                                                                                                                                          540
                                                                                                                                                                                                                                                                                        599
                                                                                                                                                                                                                                                                                                                                     629
                                                                                                                                                                                                                                                                                                                                                                                                                                  769
                      CCAGAGAGAGCAAATCGAAGCGTGGGAGGCACCCCCATTGCTCTCCTC
                                                                                                                    a--cccttccccaccaggctaggcccccacacctgggggacccct
                                                                                                                                                                                                                                                                                                                                                           ty sequence stop: 766.
ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:12386017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NIH_MGC_88
nce.
```

st

H

7

56

-7 m m _7

> S ゴ

-2001 2 5',

EST 07-MAY-2 IMAGE:4800482

linear

Euteleostomi

(MGC)

DNA

```
/db_xref="taxon:9606"
/clone=lib="NIH_MGC_88"
/clone_lib="NIH_MGC_88"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
                                                                                         7;
                                                                                                                           120
                                                                                                                                     203
                                                                                                                                                180
                                                                                                                                                           263
                                                                                                                                                                      240
                                                                                                                                                                                 323
                                                                                                                                                                                           300
                                                                                                                                                                                                                                                          479
                                                                                                                                                                                                                                                                                539
                                                                                                                                                                                                      382
                                                                                                                                                                                                                 360
                                                                                                                                                                                                                                      419
                                                                                                                                                                                                                                                                                                      595
                                                                                                                                                                                                                            441
                                                                                                                                                                                                                                                 501
                                                                                                                                                                                                                                                                      560
                                                                                                                                                                                                                                                                                            620
                                                                                                                                                                                                                                                                                                                 680
                                                                                                                                                                                                                                                                                                                            655
                                                                                                                                                                                                                                                                                                                                       740
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                  714
                                                                                                                                                                                                                                                                                                                                                             800
                                                                                                    9
                                                                                                     lagggcc
                                                                                                                          cccgca
|||||||
                                                                                                               AGGGCC
                                                                                                                                                                      agagca
                                                                                                                                                                                                                                                                                       AGTICA
                                                                                                                                                                                                                       |||||||||||GGAGAA
                                                                                                                                                                                                                                                         ggagaa
                                                                                                                                                                                                                                    lilli
                                                                                                                                                                                 AGAGCA
                                                                                                                                                                                                                                                                                 gttca
                                                                                                                                                                                                                                                                                                                          ACCCT
                                                                                         6
                                                                               04;
                                                                                                                                                                                                                                                                               Length
                                                                                         Indels
                                                                             Score 578.6; DB 10;
Pred. No. 1.8e-69;
0; Mismatches 34;
                                                                             Query Match
Best Local Similarity 94.0%;
Matches 678; Conservative
                                                        Ø
                                                        50
                                                                                                                                                                                                                                                                                                                                                                                801
                                                                                                                                                                                                                                                                                                                                                                               Ö
                                                                                                   Н
                                                                                                              84
                                                                                                                                              121
                                                                                                                                                        204
                                                                                                                                                                    181
                                                                                                                                                                              264
                                                                                                                                                                                                    324
                                                                                                                                                                                                                                                                                         561
                                                                                                                                    144
                                                                                                                                                                                         241
                                                                                                                                                                                                               301
                                                                                                                                                                                                                          383
                                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                    502
                                                                                                                         61
                                                                                                                                                                                                                                               442
                                                                                                                                                                                                                                                                                                     540
                                                                                                                                                                                                                                    361
                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                                                                                                               621
                                                                                                                                                                                                                                                                                                                          596
                                                                                                                                                                                                                                                                                                                                                929
                                                                                                                                                                                                                                                                                                                                                          741
                                                                                                                                                                                                                                                                                                                                     681
                                                                                                                                                                                                                                                                                                                                                                     715
                                                                                                                                                                                                                                                                                                                                                                                801
                                                       BASE CO
                                                                                                             g
                                                                                                                        δ
                                                                                                                                   a
                                                                                                                                                         g
                                                                                                                                                                              g
                                                                                                                                                                                                    qq
                                                                                                                                                                                                                         g
                                                                                                   õ
                                                                                                                                                                                         ò
                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                    ДQ
                                                                                                                                                                                                                                                                                         Op
                                                                                                                                                                    ŏ
                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                               D
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                          P
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                ò
```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4800482"
/clone_lib="NCI_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
Technologies and the state of t
                                                                                                                                                                                     Hommos sapiens

Hommos sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 762)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA

Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10691 row: j column: 03

High quality sequence stop: 762.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaagcctagtgggcctagacccctcctcccatggctagaagtggggcctgcaccatacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gggaggcaccccattgctctcctccaggggcagaacatggggaggggactagatgggca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 762;
                                     cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 566; DB 10;
Pred. No. 9.4e-68;
0; Mismatches 26;
             sapiens c
             762 bp
Homos
                                     NCI_CGAP_Skn3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                    GI:13966642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.5%;
ilarity 94.8%;
Conservative
BG698896
602703313F1 NCI
MRNA sequence.
BG698896
BG698896.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Similarity 704; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
       LOCUS
DEFINITION
                                                                                                                                                                                                  ORGANISM
                                                                                   ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
```

11;

Gaps

13;

Indels

718

9

778

118

838

178

237

838

1018

355

RESULT 1 BG698896

296

```
1. .902
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DI026Y124"
/clone=lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: Not1; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
61 a 297 c 278 g 156 t 10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                             1258
                                                                    533
                                                                                                                        590
                                                                                                                                                 1318
                                                                                                                                                                         649
                                                                                                                                                                                                                                                                                                                                    AL546822
AL546822 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI026YI24 5
prime, mRNA sequence.
AL546822
AL546822.1 GI:12680311
                                                                                                                                                                                                   137
                 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 uteleos
                                          tectec
||||||
rccrec
                                                                                             Cacccc
CACCCC
     GGGCA
                                                                                                                                                Homo
                                      cccactcccacttccaggattgtggtttggattgaaaccaagtttacaagtagac
                                                                                                                                           902;
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web : www.genoscope.co
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 902)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 553.2; DB 9;
Pred. No. 4.9e-66;
3; Mismatches 37;
                                                                                                                                                                                                                                                accectgacettettgactte 1401
                                                                                                                                                                                                                                                          710 CCCCGGACTTCTTGATTCCCTTC 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%;
91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 749; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                      EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
            416
                                                                                                                  534
                                                                                         1199
                                                                                                                                            1259
                                                                                                                                                                   591
                                                                                                                                                                                              1319
                                                                                                                                                                                                                      650
                                                                                                                                                                                                                                                1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                             RESULT 1
AL546822
                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                     Qγ
                                                             g
                                                                                                                 qq
                                                                                         δy
                                                                                                                                            ò
                                                                                                                                                                   qq
                                                                                                                                                                                              δy
                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
2001
                      270
                                             330
                                  246
                                                        306
                                                                                         447
                                                                   387
                                                                              366
                                                                                                    426
                                                                                                               507
                                                                                                                          486
                                                                                                                                     999
                                                                                                                                                546
                                                                                                                                                           624
                                                                                                                                                                      909
                                                                                                                                                                                            999
                                                                                                                                                                                                                              803
 21
                                                                                                                                                                                                                                                                                                                linear EST 27-MAR clone IMAGE:4667555 5
                                                                                                                                                                                                       74
                                                                                                                                                                                                                                                                                                                                                              Euteleos
Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                    Coll
                                                                                                                                                                                                                                                                                                                                                              Vertebrata
                                                                                                                                                                                                                                                                                                                                                                                                               CLONETECH Laboratori
                                                                                                                                                                                                                                                                                                                                                                                   Gene
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 547)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laborate
                                                                                                                                                                                                                                                                                     881
                                                                                                                                                                                                                                                                                                                mRNA
cDNA
                                                                                                                                                                                                                                                                         547 bp m
                                                                                                                                                                                                                                                                                                                      60 Homo
                                                                                                                                                                                                                                                                                                                                      GI:1346124
                                                                                                                                                                                                                                                                                                               BG499730
602545144F1 NIH_MGC_6
mRNA sequence.
BG499730
BG499730.1 GI:134612
                                                                                                                                                                                                                                                                                                                                                  human
57
          127
                                                      247
                                                                                        388
                                                                                                  367
                     214
                                187
                                           271
                                                                  331
                                                                            307
                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                              448
                                                                                                                        427
                                                                                                                                    508
                                                                                                                                              487
                                                                                                                                                                    547
                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                          567
                                                                                                                                                                               625
                                                                                                                                                                                           607
                                                                                                                                                                                                      685
                                                                                                                                                                                                                 667
                                                                                                                                                                                                                            744
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                       727
                                                                                                                                                                                                                                                  804
                                                                                                                                                                                                                                                             785
                                                                                                                                                                                                                                                                        864
                                                                                                                                                                                                                                                                                    842
                                                                                                                                                                                                                                                                                                    RESULT 1
BG499730
                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                               LOCUS
         q
                     ò
                                qq
                                                       g
                                                                            g
                                                                                                  g
                                                                                                                         g
                                           9
                                                                  ò
                                                                                        à
                                                                                                                                              g
                                                                                                                                                          ò
                                                                                                              à
                                                                                                                                    ô
                                                                                                                                                                    a
                                                                                                                                                                                ò
                                                                                                                                                                                           qq
                                                                                                                                                                                                                 Ω
                                                                                                                                                                                                                                       Op
                                                                                                                                                                                                      ò
                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                         δ
```

.rst

7

-09-733-756

ns

```
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Clone_lib="NIH_MGC_60"
// Lissue_type="adenocarcinoma"
// Lissue_type="adenocar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1137
                                                                  þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                 ion can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gaageg
||||||||||
GAAGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
DNA Sequencing by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution informatiound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1476 row: g column: 12
High quality sequence stop: 537.
Location/Qualifiers
1. .547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 530.2; DB 10;
Pred. No. 7.3e-63;
); Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%;
illarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
543; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gccccc 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 543
                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1437
                                                                                                                                                                     FEATURE
```

ò

ô

a

g

Q

g

g

ò

ò

g

ò

qq

ò

g

ò

d

δ

```
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 496)

S Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

'M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

L Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-270001
Email: asimpson@ludwig.org.br.
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-NN1187-11100-478-a06&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 495.
Location/Qualifiers
I. .496
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN1187"
                                                                                                     EST 22-JAN-2001
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: nervous_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sao Paulo-SP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctccggggagaagccggtccccactctccccagttcaccatgggccccaatgtgaagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caacgtgctggaagactttgagggagagaccctcaggtgcccaagcttgagaagagcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 496;
                                                                                               BF953157
CM3-NN1187-111100-478-a06 NN1187 Homo sapiens CDNA, BF953157
BF953157.1 GI:12370432
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 439.2; DB 10;
Pred. No. 1.6e-50;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.2%;
ilarity 97.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
466; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brazil
541 GGCCCCC
                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 466
                                                          RESULT 14
BF953157/c
                                                                                                                      DEFINITION
                                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

7

S

```
SM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 420)
S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
L Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                         xw97ell.xl NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2835980 3', mRNA sequence.
BE138904
BE138904.1 GI:8601404
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2835980"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. 11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1397
681
                         257
                                                   741
                                                                           197
                                                                                                     801
                                                                                                                              137
                                                                                                                                                        861
                                                                                                                                                                                78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
ttcct
||||||
                                                tatatataatgtacagacagacagagtcccttccctcttaacccctgacctttcttga
                                                                                                                                                                                                         917
                                                                                                                                                                                                                                  22
                                                                                                                                                                                                       tececeaegtagggeaetgtagtggaeeaageaeggggaeageeatgggteeegg
Length 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 416.8; DB 9;
Pred. No. 1.8e-47;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     р
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .ch 23.9%;
il Similarity 99.5%;
41%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                       RESULT 15
BE138904/c
                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                         862
                        316
                                                                         256
                                                                                                    742
                                                                                                                             196
                                                                                                                                                      802
                                                                                                                                                                               136
                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1278
                                                  682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                LOCUS
                        qq
                                                                         g
                                                                                                                             g
                                                                                                                                                                               q
                                                  õ
                                                                                                                                                      ò
                                                                                                                                                                                                                                  a
ð
                                                                                                                                                                                                         ò
                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
```

```
1457
                                   1517
                                                          1577
                                                                                   1637
                                               181
                                                                                                          169.
301
                                                                       121
           cttcccttcagcttcagacccttccccaccaggctaggcccccacacctgggggacc
                                                                                  TATATATAATGTACAGACAGACAGAGTCCCTTCCCTTTAACCCCCTGACCTTTCTTGA
                                   gagaccgtaaaacaacagcgcccctcccttccagccctgagccgggaaccatctccag
                                                                                                          360
           1398
                       300
                                   1458
                                               240
                                                           1518
                                                                       180
                                                                                  1578
                                                                                              120
                                                                                                                     9
                                                                                                          1638
                       a
                                                                       g
                                                                                              g
                                   ò
                                               q
                                                           ò
                                                                                   à
                                                                                                          ò
```

Search completed: July 13, 2002, 09:10:59 Job time: 1839 sec $\boldsymbol{\dashv}$

```
cell updates/sec
                                                                                                                                                                                aaaaa 1743
                                   July 13, 2002, 08:43:30 ; Search time 216.15 Seconds (without alignments) 13844.931 Million cell
                                                                             ..aaaaaaaaaaaaaaa
                                                                                                                          3472872
       Ltd.
4.5
Compugen
                                                                                                                        hits satisfying chosen parameters:
                                                                                                            1736436 seqs, 858457221 residues
version .
                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                          model
                                                                            1 gctgctgctgctgctgc..
                                                                                                Gapext 1.0
                        nucleic search, using sw
GenCore (c) 1993
                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                         US-09-733-756-1
1743
                                                                                        IDENTITY_NUC Gapop 10.0 ,
     Copyright
                                                                                                                                                                                          of
                                                                      score:
                                                                                         Scoring table:
                                                                                                                         Total number
                        OM nucleic
                                                                           Sequence:
                                                                                                            Searched:
                                                                                                                                                                                   Database
                                                                     Perfect
                                     Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Epn cransmembrane	Human hek-L protei	Human colon cancer		Human secreted pro	Human LERK-6 polvo	Chicken elf-1 cDNA	cDNA encoding an a	Mouse Elf-1 cDNA.
SUMMARIES	1		C0000144	AAQ85887	AAA01637	AAA00162	AAC03424	AAX32767	AAT15009	AAV42927	AAT15008
		16.	OT	16	21	21	21	20	17	19	17
	Length DB	1070	2 2 4	1037	715	257	358	642	783	783	1809
gap.	Query	7 Y Y		ς.	٠	4	1.		8.6		
	Score	070	•	7.	7.	ď.		6	149.2		
	Result No.	 	1	7	m	4	ស	9	7	8	6

LERK-6 exon. Homo Exon sequence of h Lerk-6 coding sequ LERK-6 coding sequ LERK-6 poly B61 cDNA sequence. B61 cDNA sequence. B61 gene. Homo sa Human PRO202 cDNA. Human PRO202 cDNA. Human pancreatic c Human pancreatic c Human differential Lerk-7 coding sequ DNA encoding novel DNA encoding novel Human AL-1 cDNA. Human hek-L protein DNA encoding novel Human polynucleoti Human secreted prohuman secreted prohuman secreted prohuman colon cancer Human secreted prohuman colon cancer Human secreted prohuman secreted pro	Human reproductive
AAV42926 AAT14010 AAX32766 AAT14009 AAX32761 AAQ24595 AAQ63770 AAC91576 AAC91576 AAC91576 AAC91576 AAT32699 AAT32699 AAT34292 AAT342006 AAT94700 AAX89617	0
110 110 110 110 110 110 110 110 110 110	22
1809 1448 11489 11489 1172 1173 1173 1173 1173 1173 1173 1173	\mathbf{c}
0	` .
139 139 128 128 128 128 128 128 135 135 135 135 136 137 137 138 137 138 138 138 138 138 138 138 138 138 138	57.8
1 H I I I I I I I I I I I I I I I I I I	45
O O	

ALIGNMENTS

```
Eph transmembrane tyrosine kinase family ligand, Efl-2 encoding DNA
                                                                                Efl-2; EHK1-L; Eph transmembrane tyrosine kinase ineurological disorder; identification; diagnosis;
                                                                                                                        Location/Qualifiers
46..750
/*tag= a
/product= Ef1-2
                 ВР
                 standard; DNA; 1070
                                                                                                                                                                                                                 94US-0327423.
94US-0222075.
94US-0229402.
94US-0299567.
                                                                                                                                                                                                   95WO-US04208
                                                                                                                                                                                                                                                            (REGE-) REGENERON PHARM INC
                                                 (first entry)
                                                                                                                                                                                                                 21-OCT-1994;
04-APR-1994;
12-APR-1994;
01-SEP-1994;
                                                                                                           sapiens
                                                                                                                                                                 WO9527060-A2
                                                                                                                                                                                                   04-APR-1995;
                                                 16-MAY-1996
                                                                                                                                                                                  12-OCT-1995
                AAT03883
                                AAT03883
                                                                                                          Ното
RESULT
AAT03883
                                                                                                                          Key
```

family ligand

SS

7

```
enotye,
lls. They
disorders.
                                                                                                         ligand
inds for
ul in
                                                              of
                                                                ŝ
                                                                                                                                                                                                ö
                                                                                                                                                                                                \sim
                                                                                                      The DNA encodes an Eph transmembrane tyrosine kinase family designated Ef1-2. Ef1-2 is useful for identifying other ligareth-1, -2, -3, Eck and Elk receptors. The ligands are useful promoting a differential function and/or influencing the phersuch as growth and/or proliferation, of receptor bearing cellmay be used in the diagnosis, and treatment of neurological contracts.
           \mathbf{p}_{\mathbf{C}}
                                                                                                                                                                                                10,
                                                              diagno
           erre
                                                                                                                                                                                                Length
                                                                                                                                                                      other
                                                               the
           sonpi
                                                              used in
                                                                                                                                                                     10
           Mai
                                                                                                                                                                    Ţ;
          ΣÌ
                                                                                                                                                                     189
           Goldfarb
                                                               receptors
                                                                                                                                                                     Ğ;
                                                                                                                                                                    334
                                                                                        English
                                                                                                                                                                    ς;
                                                             family
          Z
                                                                                                                                                                    341
           Gale
                                                                                       28pp;
                                                                                                                                                                     A;
                                                             h bind Eph
disorders
                                                                                                                                                                    BP; 196
         S
                                    9
         Davis
GD;
                                  95-358635/46
AAR82605.
                                                                                      3;
                                                                                     sclosure; Fig
                                                             Ligands which
neurological c
                                                                                                                                                                    Sequence 1070
        Irich TH,
                                   199
        Aldrich
Yancopou
                                                            gands
                                           Ø
                                           SD
```

ij 240 120 180 300 360 239 287 407 420 347 467 480 527 540 587 909 647 099 707 720 Gaps 9 17 ctgcg |||||| ctgcg cgca ggctt ||||||| |ggctt cacta ||||| tegt ||||| |tegt aggt ||||| |aggt ||||| tggc cctg ||||| |cctg Jagaa gagaa tcac cccgca tggc 12; ctgctgcgcctccacatcgcactccggggagaagccggtccccactctccccagt Indels Score 949.2; DB 16 Pred. No. 3.8e-181; ; Mismatches 18; ö Match 54.5%; Local Similarity 97.0%; Les 976; Conservative Ď g Н 9 120 tches 61 121 180 181 240 288 301 $\boldsymbol{\omega}$ 361 408 421 468 528 541 601 481 588 648 661 34 Que Best Mato qq qq g ð ò g q ò g ŏ ò ò a ò d g d õ à ò a ð Q

767

```
1007
             827
                          840
                                       887
                                                    900
                                                                              096
                                                                947
 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is that of a clone encoding hek-L protein, a protein that can bind hek (a cell surface receptor tyrosine kinase). Hek-L is the first known ligand for hek and can be used to study cellular processes regulated by hek (which may be involved in tumorigenesis)
New isolated DNA encoding hek-L protein or its fusion products useful as assay reagent or for carrying therapeutic and diagnostic compounds to leukaemia cells.
                                                                                                                                                                                                        tumorigenesis
                                                                                                        1006
                                                                                                       receptor;
                                                                                                                                                     ВР
                                                                                                                                                                                                        kinase
                                                                                                                                                    mRNA; 1037
                                                                                                                                                                                                                                   Location/Qualifiers
83..799
/*tag= a
83..139
                                                                                                                                                                                           A2
                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                           cDNA clone
                                                                                                                                                                                                        surface; tyrosine
                                                                                                                                                                                                                                                                                                                                93US-0109745.
93US-0114426.
93US-0161132.
94US-0240124.
                                                                                                                                                                                                                                                                                                                    94WO-US09282
                                                                                                                                                    ţ0
                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                       Ω
                                                                                                                                                                                                                                                                                                                                                                               DP
                                                                                                                                                    AAQ85887 standard; cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                        34; 45pp;
                                                                                                                                                                                                                                                                                                                                                                              Cerretti
                                                                                                                                                                                                                                                                                                                                                                  (IMMV ) IMMUNEX CORP
                                                                                                                                                                                           protein
                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                           1995-106811/14
)B; AAR71481.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                              SS
                                                                                                                                                                                                        cell
                                                                                                                                                                                                                                                                                                                                20-AUG-1993;
30-AUG-1993;
03-DEC-1993;
09-MAY-1994;
                                                                                                                                                                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                              Beckmann MP,
                                                                                                                                                                                                                                                                                                                    17-AUG-1994;
                                                                                                                                                                                           Human hek-L
                                                                                                                                                                              03-OCT-1995
                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                       peptide.
                                                                                                                                                                                                                                                                                          W09506065-A
                                                                                                                                                                                                        Ligand; cel
immunogen;
                                                                                                                                                                                                                                                                                                       02-MAR-199
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                 AAQ85887
                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
            768
                                                                                                                    1008
                                      828
                                                    841
                                                                                          948
721
                                                                888
                                                                             901
                                                                                                                                                                                                                           Ношо
                          781
                                                                                                       961
                                                                                                                                                                                                                                                                       mat_
                                                                                                                                       RESULT
AAQ85887
                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                           WPI
                                                                                                                                                    셤
                                       d
                                                                g
                                                                                          g
                                                                                                                    qq
                          à
                                                    ŏ
                                                                              ò
                                                                                                        à
```

```
in immunogen for antibody production, as a reagent for sk or hek-L in in vitro assays, to determine binding of i, to purify hek proteins, and to carry diagnostic or lents to particular leukaemia cells that express the hek k-L also binds the elk tyrosine kinase receptors.
  It is also an indetecting hek on hek proteins, the cytotoxic agentantigen. Hek-L See also AAQ858
```

```
ö
                                     120
                                                 180
                                           216
                                                        276
                                                               240
                                                                     336
                                                                            300
                                                                                         360
                                                                                               456
                                                                                                     420
                                                                                                            516
                                                                                                                               540
                                                                                                                         576
                                                                                                                                     636
                                                                                                                                            009
                                                                                                                                                  969
                                                                                                                                                         099
                                                                                                                                                                     756
                                                                                                                                                                                   780
                                                                                                                                                                                                840
                 Gaps
                                                                                                                                                                                         876
                                                                                                                                                                                                            900
                       9
                                                                                                                                                                                                                   966
                       agggcc
                                        IIIIII
                                                  cccgca
                                                                            gggctt
                                                                                                                  gttcgt
|||||||
gttcgt
                                                               agagca
                                                                                  gggctt
                                                                                                           gtacta
                              agggcc
                                                                                                                                  ctggc
                                                                                                                                                                                   laggga
                                     cctgcg
                                                        cccgca
                                                                      agagca
                                                                                                                                          ctggc
                                                                                         ggagaa
                                                                                                     gtacta
                                                                                                                               ttcac
                                                                                                                                                                                                catct
                                                                                               ggagaa
                                                                                                                                                                                                             11111
                                                                                                                                                                                          aggga
                                                                                                                                                                                                      catct
                                                                                                                                                                                                                    cgggg
          .037;
                 0;
                       ttctcg
||||||
                                                                                                                                                                                                           tg__
                                                        tg
                                                                                                    tcccccag
tcccccag
                                                                                                                                                                                  Ca
                                                                                                                                                                                                Lengt
                 Indel
                                                                                        other
                                                 tat
|--
                                                             ctct
||||||
                      gat
||||
gat
                                                                                                                               tatctgg
|||||||||
tatctgg
                                                                                                                                                                                                      999
          9 .. ..
0
                                                                                                                                                                                                <u>6</u>—
          2 2
                                                                                                                                                                                                tgg
||||
tgg
          DB
4e-17
H
                                                                                                                                                                                               tgggcctagacccrtcctcccatggctagaag
         Score 917.8;
Pred. No. 7.4e
0; Mismatches
                                                 170
                                                                                                                              S
37
                                                 ygtgaacgt
||||||||||||||
ygtgaacgt
3
ີ່:
                O
3
                                                 rtgcago
||||||||||
|tgcago
         52.7%
imilarity 99.8%
; Conservative
æ
Ä
                                                 187
                                                                                                                                                                     BP;
                                                                                                                                                                     tcg
||||
tcg
                                                                                        1037
                                                             ctgctgc
|||||||||
ctgctgc
                                                                           tacgt
||||||
|tacgt
         Query Match
Best Local Sig
Matches 919;
                                                                                                                                                                    9tgg
||||||
9tggg
                       ctg
|-|-
edneuce
                                                                                                                                                                                                     ag
                       ₽-
                             g
                                                 Φ
                                                       φ.
                                                                           ρ
                                                                                 δ
                                                                                                                                                                                                            ρ
                                                                                                                                                                                                               <del>-</del> و
                                   61
                                                                   277
                                                121
                                                             181
                                                                           241
                                                                                 337
                                          57
                                                                                       301
                                                                                              397
                                                                                                    361
                                                                                                          57
                                                                                                                       517
                                                                                                                                    577
                                                                                                                                           541
                                                                                                                                                 37
                                                                                                                                                        601
                                                                                                                 21
                                                                                                                              81
                                                                                                                                                              697
                                                                                                                                                                    661
                                                                                                                                                                           757
                                                                                                                                                                                 721
                                                                                                                                                                                              81
                                                                                                                                                                                                     877
                             셤
                                   δ
                                          qq
                                                       g
                                                                    g
                                                ò
                                                             ò
                                                                                 q
                                                                                              g
                                                                          ò
                                                                                                           a
                                                                                       õ
                                                                                                    ò
                                                                                                                       g
                                                                                                                                    qq
                                                                                                                                                 Db
                                                                                                                 ò
                                                                                                                              ò
                                                                                                                                           Ω
                                                                                                                                                                           a
                                                                                                                                                                                        g
                                                                                                                                                                    ò
                                                                                                                                                                                                     g
                                                                                                                                                                                 à
```

Η;

mammalian

Polynucleotide library used to determine cancerous states of cells -

2000-126369/11

WPI;

586; 1097pp; English

Claim 1; Page

```
Labat
                                                                                                         polynucleotide sequence SEQ ID NO:1628
                                                                                                                        Human; colon cancer; tumour; diagnosis; gene expression product;
probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                        Garcia PD, Sudduth-Klinger
Kennedy GC, Pot D, Kassam A;
t, Dickson M, Drmanac S, Lak
Tones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                               Randazzo F, Kennedy (
Crkvenjakov R, Dicksc
Garcia V, Jones LW,
                                                                                                                                                                                                                                                                                                        Innis MA,
                                                          ΒP
                                                                                                        line
                                                         715
                                                                                                                                                                                                                               98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
99WO-US10602
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                         <sub>د</sub>,
                                                          CDNA;
                                                                                                         cell
                                                                                                                                                                                                                                                                                                         Escobedo
                                                                                                                                                                                                                                                                                                                                Kita D,
                                                                                                                                                                                                                                                                                                                Giese K,
rmanac R,
                                                                                                                                                                                                                                                                                 CORP.
                                                         standard;
                                                                                                         cancer
                                                                                                                                                                                                                                                                                                                        Drmanac
                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON COI
(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                        Lamson G, Drr
Leshkowitz D,
                                                                                                                                                                                                                               14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                WO9958675-A2
                                                                                                                                                                                                                                                                                                       Williams LT,
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                13-MAY-1999;
                                                                                        19-MAY-2000
                                                                                                        Human colon
                                                                                                                                                                                                18-NOV-1999
                                                                         AAA01637;
                                                        AAA01637
                                                                                                                                                                                                                                                                                                                Reinhard
                997
901
                                         RESULT
                                                AAA01
               qq
                                                                                                                               ΩI
```

AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
libraries constructed from human colon cancer cell lines. The present
invention also describes a method of detecting differentially expressed
genes correlated with a cancerous state of a mammalian cell, comprising
detecting at least one differentially expressed gene product in a test
sample derived from a cell suspected of being cancerous, where detection
of the differentially expressed gene product is correlated with a
cancerous state of the cell from which the test sample was derived.
The polynucleotides sequences can be used in a method for detecting
differentially expressed genes correlated with a cancerous state of a
mammalian cell. The polynucleotides can also be used as probes for
detecting and mapping related genes. They can be used in diagnosis and
prognosis of diseases and disorders (e.g. identification of
prognosis of diseases and disorders (e.g. identification of
pre-metastatic or metastatic cancerous states, stages of cancer, or
responsiveness of cancer to therapy). This is particularly for breast
cancer, oestrogen receptor-positive breast cancer, oestrogen receptoroegative breast cancer, lung cancer, and colon cancer.

other; T; 69 180 125 ວ່ 188 Ą. BP; 715 Sequence

Length 71 21; 447.8; DB 2 No. 1.2e-80; Score Pred. 25.7%; 95.3%; Query Match Best Local Similarity

```
5
           Jtggtt 1225
                                  1285
                                                         1345
                                                                               1405
                                                                                                     1465
                                                                                                                           1525
                                                                                                                                                 1583
                                                                                                                                                                       1641
                                                                   230
                       116
                                             170
                                                                                         290
                                                                                                                350
                                                                                                                                      410
                                                                                                                                                            470
                                                                                                                                                                                   ttggg 530
 Gaps
                                                                                                                                                                                            ||||||
|atata
                      tggtt
                                                                                                                                                acctt
|||||||
acctt
                                  ggatg
                                                       tggcc
                                                                                                                tggcc
                                                                                                                           accgt
                                                                                                                                                                                                                                                                      10:153
                                             ggatg
                                                                             tttgg
                                                                                                                                       accgt
                                                                                                                                                                                                                                                                                                                                                                                                          Sudduth-Klinger
Pot D, Kassam A;
                                                                                                                                                                                                                                                                                colon cancer; tumour; diagnosis; gene expression product; detection; cancerous state; metastasis; identification; cancer; oestrogen receptor-positive breast cancer; therapy yen receptor-negative breast cancer; ss.
 7;
          tcagettcagaccettceceaeggetaggeeceeeaeaetgggggaeeee
                                                                                                                         aaaacaac-agcgcccctcccttccagccc-tgagccgggaaccatctcccaggalliiliiliiii
                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                           cancer; t
 Indels
                                                                                                                                                                                                                                                                      sednence
18;
                                                                                                                                                                                                                                                                                                                                                                                                           CC,
                                                                                                                                                                                                                                                                                                 lung
                                                                                                                                                                                                                                                                                                                                                                                                           , Garcia
Kennedy G
                                                                                                                                                                                                                                                                     cell line polynucleotide
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           MA,
                                                                                                                                                                                                                                                                                                                                                                                                                 Ē
                                                                                                                                                                                                                                                                                                                                                                                                           J, Innis
Randazzo F
                                                                                                                                                                                                                                    BP
ô
                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                        98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
                                                                                                                                                                                                                                                                                                                                              99WO-US10602
                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                    CDNA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Escobedo
Giese K,
                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                      Human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                         CHIRON
HYSEQ I
                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                                                                                                                                        -1998;
-1998;
-1998;
-1998;
                                                                                                                                                                                                                                                          19-MAY-2000
                                                                                                                                                                                                                                                                                                                                             3-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                           Ľ,
                                                                                                                                                                                                                                                                                                                                  8-NOV-1999
512
                                                                                                                                                                                                                                                                                                                                                                                                         Williams
Reinhard
                                                                                                                                                                                                                                    AAA00162
                                                                                                                                                                                                                                                                                                                       WO995867
                                                                                                                                                                                                                                                                                                                                                                                         (CHIR) (HYSE-)
                                                                                                                                                                                                                                                                                                                                                       14 - MAY -
15 - MAY -
15 - MAY -
21 - OCT -
27 - OCT -
                                                                                                                                                                                                                                                                                           breast
oestrog
                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                      probe
                                                                                                                                                                                                                                                                                                            Ношо
                                                                                                   1406
          1166
                                 1226
                     52
                                            111
                                                                  171
                                                                                                                          1466
                                                                                                                                                1526
                                                                                                                                                                                            1642
Matches
                                                       286
                                                                             346
                                                                                         231
                                                                                                              291
                                                                                                                                     351
                                                                                                                                                           411
                                                                                                                                                                                  471
                                                                                                                                                                                                       531
                                                                                                                                                                      1584
                                                                                                                                                                                                                              9
                                                                                                                                                                                                                       SULT
                                                                                                                                                                                                                        RESULT
AAA001
                                            g
                                                                                                                                                                                                                                   ò
                                                                  D
                                                                                         qq
                                                                                                               g
                                                                                                                                     g
                                                                                                                                                           a
                                                                                                                                                                                  Dp
                                                       ò
                                                                              ò
                                                                                                    ò
                                                                                                                          ŏ
                                                                                                                                                δ
                                                                                                                                                                      δ
                                                                                                                                                                                             ô
                                                                                                                                                                                                       g
```

```
AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA isolation;
                                                             mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1345
                                                                                                                                                                                                                                                                                                                                                                                                           ccctgtttacagcaataagcacgtcctcccccactcccacttccaggattgtggtt 1225
                                                                                                                                                                                                                                                                   pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
      Labat
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                             of
     M, Drmanac
Stache-Crain
                                                               states
                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                                                                                                                                                                                                                                       cancer, and colon cancer
                                                             to determine cancerous
                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                              0 other;
                                                                                                                                                                                                                                                                                                                                                       Score 252.2; DB 21;
Pred. No. 1.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted
     Dickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO: 3422
     R, Dicksc
Jones LW,
                                                                                                                                                                                                                                                                                                                             66 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence tag;
mapping; ss.
                                                                                              1097pp; English.
     Crkvenjakov
Garcia V,
                                                                                                                                                                                                                                                                                                                              59 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST,
                                                                                                                                                                                                                                                                                                       breast cancer, lung
                                                                                                                                                                                                                                                                                                                              ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358
                                                              nseq
                                                                                                                                                                                                                                                                                                                                                              14.5%;
ilarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcagcttcagacccctt 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                             257 BP; 58 A; 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed chromosome
                                                            Polynucleotide library cells -
R,
D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac
D, Kita
                                      2000-126369/11
                                                                                              216;
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST;
                                                                                              Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                         Local Sim
hes 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000
           Leshkowitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                        negative
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC03424
      Lamson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1406
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                            1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC03424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
   á
                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC
XX
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

```
ved from
full length
                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                  procedures
                                                                                                                                                                                                                                             T) for and for
                                                                                                                                                                                                                                              tag (5' EST)
to 5'ESTs and
                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' Fobtaining cDNAs and genomic DNAs that correspond to 5'ESTs diagnostic, forensic, gene therapy and chromosome mapping
                                                                                                                                                     ij,
                                                                                                                                                                                                                                                                                                                   + CD-ROM; English.
                                                                                                                                                    Giordano
                                                                                                                                                     À
                                                                                                                                                    Duclert
                                      2000EP-0200610
                                                                          99US-0122487
                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 3422; 71pp
                                                                                                                                                    ٦,
                                                                                                                                                                                     2000-500381/45.
                                                                                                                                               Dumas Milne Edwards
                                                                                                                                                                                                       P-PSDB; AAG03418
                                                                                                             (GEST ) GENSET
                                    21-FEB-2000;
                                                                          26-FEB-1999;
  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vectors
```

472 gagaatcgctgtttctccacgcccactcacaacctgcactggaagtgtctgaggatgaag 190 Gaps gagtactactacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaag ö 358; Length Indels 637 0 other; 21; Score 205.8; DB 21 Pred. No. 3.5e-32;); Mismatches 12; Ţ, 358 BP; 74 A; 102 C; 122 G; 60 ; 11.8%; larity 94.7%; Conservative Local Similarity les 213; Conser Sequence Query Match Best Loc Matches 413 131 191 533 251 593

ДQ

ŏ

qq

qq

οŻ

ag

ò

250

355

LERK-6 polypeptide; hek receptor; elk receptor; human; murin cell proliferation; neural growth; neural tissue; neurologic neurodegenerative; excitotoxicity; ss. ВP polypeptide encoding cDNA. 642 standard; cDNA to mRNA; (first entry) Human LERK-6 24-JUN-1999 AAX32767; AAX32767 9 RESULT AAX32767

sapiens

injury; disease;

e;

The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the hek or elk receptor. The ligand and receptor complex may be involved in treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neural diseases, either chronic or acute. LERK-6 may be employed in treating consuctive conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a ggagggggcgctgggaaaccggcatgcggtgtactggaacagctccaaccagcacctgcgg gecegegecaacteggacegetacgeegtetactggaacegeageaaceceaggtteeac gggctacaccgtgcaggtgaacgtgaacgactatctg 642; 45; Length Indels A; 247 C; 193 G; 105 T; 0 other; DB 20; 158; Score 149.2; D Pred. No. 9e-21 ; Mismatches encoding a human LERK-6 polypeptide. English ; 0 New cytokine designated LERK-6 97US-0920440 ch 8.6%; 1 Similarity 61.8%; 329; Conservative 46pp; (IMMV) IMMUNEX CORP WPI; 1999-243567/20 Sequence 642 BP; 97 42; -PSDB; AAY06822 Page 9-AUG-1997; WO9910495-A1 Cerretti DP; 04-MAR-1999 27-AUG-1998 cgaga-Query Match Best Local S Matches 329 Claim 3; CDNA 88 122 62 148 208 224 247 164 284 307 341 367 qq d Q q ò g ò ò δ a 원 ð

ö

4

163

207

147

87

246

Jul

9

Length 783

17;

DB

Score 149.2;

8.68;

```
Best Local
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
5'UTR
                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3'UTR
                                                          96
                                                                          169
                                                                                          136
                                                                                                         229
                                                                                                                         196
                                                                                                                                         280
                                                                                                                                                         256
                                                                                                                                                                        325
                                                                                                                                                                                                       385
                                                                                                                                                                                                                       373
                                                                                                                                                                                                                                      445
                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                                                                                     505
                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                     AAV42927
                                                                                                                                                                                                                                                                                             RESULT
                                           <del>Q</del>
                                                                          g
                                                          ò
                                                                                                         qq
                                                                                                                                                                        Ω
                                                                                          ò
                                                                                                                         ò
                                                                                                                                         g
                                                                                                                                                         ô
                                                                                                                                                                                        à
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                      ò
   457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis
   ggaag
                   agaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A chicken cDNA clone (AAT15009) codes for a novel EPH receptor light (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from a day-3 chick embryo cDNA library using mouse Elf-1 cDNA (see AAT15008) as probe. The cDNA can be used for the product recombinant Elf-1, in the breeding of transgenic animals, for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                        gene therapy
                                 6
                                                 æ
20
                                                 53
                               ine and chicken EPH receptor ligand, Elf-1 - useful in
treatment of disorders associated with the Elf-1 gene,
entia, tachycardia , etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                      receptor ligand; dementia; tachycardia; transgenic animal; ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 783 BP; 140 A; 270 C; 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107pp;
                                                                                                                                                                                                                                                                                                                                        95WO-US11869
                                                                                                                                                                                                                                                                                                                                                       95US-0393462
94US-0308814
                                                                                                                                                                                                                                                                           /*tag= e
1471..1476
/*tag= f
                                                                                                                        entry)
                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                             ಥ
                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                             /*tay-
149..685
                                                                                                                                                                                                                                                                  ..783
                                                                                        CDNA;
                                                                                                                                                                                                                            /*tag=
86..148
                                                                                                                                                                                                                    86..688
                                                                                                                                                                                                                                                                                                                                                                               (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                    1..85
/*tag=
                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87-88;
                                                                                                                                                     Elf-1; EPH receptor
                                                                                                                      (first
                                                                                                                                                                                                                                                                   989
                                                                                                                                                                                                                                                                                                                                                                                                             1996-188446/19.
B; AAR94767.
                                                                                                                                       CDNA
                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                              Flanagan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Page
                                                                                                                                      Chicken elf-1
                                                                                                                                                                                                                                                                                                         WO9609384-A1
                                                                                                                                                                                                                                                                                                                                                       27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                                        19-SEP-1995;
                                                                                                                       02-JUL-1996
                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                         28-MAR-1996
                                                                                                                                                             diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine and and treatme
                                                                                                      AAT15009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   dementia,
                                                                                     AAT15009
                                                                                                                                                                                                                                                                                                                                                                                              Ή,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 199
P-PSDB;
                                                                                                                                                                             Gallus
                                                                                                                                                                                            Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                              Cheng
                                                                                                                                                                                                                                                                 3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
401
                 427
                                               487
                                                                                                                                                                                                                    CDS
                                                                               AAT15009
                                                                        RESULT
                g
                                               a
                                                                                                                                                                            OS XX XX EH FT FT FT FT FT FT
                                ò
                                                                                                      XXXX
                                                                                                                                      ΘE
```

```
2;
                                                                                             228
                                                                                                                 195
                                                                         'n
                                                                                                                                      279
                                                                                                                                                                                                  312
             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken; EPH receptor ligand; Elf-l; mek-4; sek-AP; tyrosine kinase ligand; B61; LERK-2; proliferation; differentiation; intracellular signalling; increased; survival; neuronal cell; neuron survival; treatment; Alzheimer's; Parkinson's; lymphatic tumomential liver; cartilage; bone formation; ss.
                                1
                              gctgctcgtgcccgtgccgctgctgctggcccaagggcccggaggggcgctggg
                                                                        aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacac
                                                    gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgaccccggcaaagtgatctc
                                                                                           ggaccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggattacac
                                                                                                               cgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaacagctcggg
                                                                                                                                                         ggtgggcccgggggccgggggccggaggcaggagcagtacgtgctgtacat
                                                                                                                                                                                                ---ggagccgctgcccgccgagcgcatggagcgctacgtcctctacat
           27;
                                                                                                                                     cgtggaggtgagcatcaatgactacctggacatctactgccctcactacga-
           Indels
 .21;
133;
 Pred. No. 9.4e-; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1..85
/*tag= a
86..688
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                  ВР
          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elf-1
                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding an avian Elf-1
63.3%;
                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0455001
94US-0308814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5US-0455001
                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product=
86..148
                                                                                                                                                                                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86..148
/*tag= c
686..783
/*tag= d
1 Similarity 63...
276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \circ
                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA;
                                                                                                                                                                                                                                                                                                                           gcccactcacaacctg
                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                        20-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5795734-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                    AAV42927;
                                                                                                                                                                                                                                                                                                                                                                                                AAV42927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ø
```

gene therapy;

-

```
A mouse cDNA clone (AAT15008) codes for a novel EPH receptor ligand, Elf-1 (AAR94766), involved in the formation and maintenance of ordered spatial arrangements of differentiated tissue. It was obtd. from an embryo mid- and hind-brain cDNA expression library using a receptor affinity probe technique with mek4-AP and sek-AP (AP = alkaline phosphatase) reagents. The cDNA is used for the prodn. of recombinant Elf-1, in the breeding of transgenic animals, for the design of diagnostic probes, and for gene (or antisense) therapy of cellular and tissue disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine and chicken EPH receptor ligand, Elf-1 - useful in diagnosis and treatment of disorders associated with the Elf-1 gene, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;
                                                                                         tachycardia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 139.6; DB 17.
larity 62.4%; Pred. No. 9.7e-19;
Conservative 0; Mismatches 134;
                                                                                         dementia;
l; ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Page 84-85; 107pp; English.
                                                                                                                                                  Location/Qualifiers
                                                                                        receptor ligand; de transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etc.
                                                                                                                                                                                                                                                                                                                                                                                           95US-0393462
94US-0308814
                                                                                                                                                                                                                                                                                                                                                                    95WO-US11869
                                                                                                                                                                                                                       /*tag= c
325.891
/*tag= d
892.1809
/*tag= e
1471.1476
/*tag= f
                                                                                                                                                                                                 q
                                                                                                                                                                             Ą
                                                                                                                                                                                    265..893
/*tag= b
265..324
                                                                                                                                                                                                                                                                                                                                                                                                                              (HARD ) HARVARD COLLEGE
                                                                                                                                                                1..264
/*tag=
265..89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ent of disortachycardia
                                          (first
                                                                                        Elf-1; EPH receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-188446/19
P-PSDB; AAR94777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flanagan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 292; Conser
                                                                  CDNA.
                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                     WO9609384-A1
                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-1995;
19-SEP-1994;
                                                                                                                                                                                                                                                                                   polyA_signal
                                                                 E1f-1
                                          02-JUL-1996
                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                            28-MAR-1996
                                                                                                     diagnosis;
                    AAT15008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ή,
                                                                  Mouse
                                                                                                                                                  Key
5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                           3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                      CDS
                                                     <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                             The present sequence encodes an avian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended itransplantation), also therapeutically in increase neuron survival (e.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atctc 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tacac 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cgcta 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504
                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                           27; Gaps
                                                                                                              eceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                getgetegtgecegtgecgetgecgetgetgectggeceaagggeceggagggegetggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||
tacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 teggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tacat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tacat
                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctgctcgccgcgatcgtcggcgtctgcgtgtggagcgacgacccggcaaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagagggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggaccgctacgccgtctattggaaccgcagcaaccccaggttccaccgcggggat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaacagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggtgggcccgggggaccgggggccggagggggggagagcagtacgtgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ggagccgctgcccgccgagcgcatggagcgctacgtcctc
                                                                                                          Nucleic acid encoding Elf-1 protein that binds to EPH-type - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgtggaggtgagcatcaatgactacctggacatctactgccctcactacga--
                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                           133;
                                                                                                                                                                                                                                                                                                                                                                                                                .4e-21;
                                                                                                                                                                                                                                                                                                                                                                 .,
E
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                C; 232 G; 141
                                                                                                                                                                                                                                                                                                                                                                                                   Score 149.2;
Pred. No. 9.
                                                                                                                                                          73-76; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA; 1809 BP
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                             Sequence 783 BP; 140 A; 270
   95US-0393462
                                                                                                                                                                                                                                                                                                                                                                                                  8.6%;
larity 63.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448
                         (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcccactcacaacctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtctccccgaacgtg
                                                                       WPI; 1998-466665/40
P-PSDB; AAW71007.
                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
276; Conser
                                                                                                                                                         Columns
27-FEB-1995;
                                                                                                                                                       Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT15008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
AAT15008
ID AAT1
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ^{Q}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
```

ж ;;

42;

Indels

Length 1809;

120

```
nase ligand;
                                                                                                                                                                                                                            cartilage
                                                                                                                                                                                                               ignalling;
nt;
              458
                                                282
                                     497
                                                           557
                                                                        339
                                                                                   617
  tatct
                         gggcc
acctg
                                                                     cccc
                                                            tcctg
                                                                                                                                                                                                          Mouse; EPH receptor ligand; Elf-1; mek-4; sek-AP; tyrosine ki B61; LERK-2; proliferation; differentiation; intracellular si increased; survival; neuronal cell; neuron survival; treatmen Alzheimer's; Parkinson's; lymphatic tumour; artificial liver; bone formation; ss.
                      encoding a mammalian Elf-1 protein.
                                                                                                                                                                                                                                                         Location/Qualifiers
1..264
                                                                                                                                                             ВР
                                                                                                                                                             CDNA; 1809
                                                                                                                                                                                                                                                                                     El f
                                                                                                                                                                                                                                                                                                                                                                    95US-0455001.
94US-0308814.
95US-0393462.
                                                                                                                                                                                                                                                                                                                                                          95US-0455001
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                               /*tag= b
/product=
892..1809
/*tag= c
                                                                                                                                                                                                                                                                                                           /*tag= d
1724..1729
/*tag= e
                                                                                                                                                                                                                                                                     Ø
                                                                                                                                                                                                                                                                                                      324
                                                                                                                                                                                                                                                                         . 894
                                                                                                                                                                                                                                                               1..264
/*tag=
265..89
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                /*tag=
255..3
                                                                                                                                                           AAV42926 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-466665/40
P-PSDB; AAW71006.
                                                                                                                                                                                                                                                                                                                                                                                                        Flanagan
                                                                                                                                                                                                                                                                                                                                                                   31-MAY-1995;
19-SEP-1994;
27-FEB-1995;
                                                                                                                                                                                                                                                                                                                polyA_signal
                                                                                                                                                                                  20-OCT-1998
                                                                                                                                                                                                                                                                                                                                  US5795734-A
                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                             18-AUG-1998
                                                                                                                                                                                                                                                                                                                                                         31-MAY-1995
                                                                                                                                                                       AAV42926
                                                                                                                                                                                                                                                                                                                                                                                                       н,
                                                                                                                                                                                                                                              Sp
                                                                                                                                                10
                                                                                                                                                                                                                                                        Key
5'UTR
                                                                                                                                                                                                                                                                                         3'UTR
          399
                                  459
                      163
                                              223
                                                                     283
                                                                                                                                                                                                                                                                                                                                                                                                       Cheng
                                                                                                       618
                                                         498
                                                                                 558
                                                                                            340
                                                                                                                                                                                               CDNA
                                                                                                                   400
                                                                                                                               678
                                                                                                                                                      26
                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                     AAV429
                                                                                                                                                RESULT
           g
                                  aa
                                                                                qq
                                                                                                       qq
                                                                                                                                                                      õ
                                                         g
                                                                                            δ
                                                                                                                              g
                                              ò
                                                                     ð
                                                                                                                   à
```

```
The present sequence encodes a mammalian EPH receptor ligand designated Elf-1. This ligand can bind to both mek-4 and sek-AP. Elf-1 is a tyrosine kinase ligand, which is linked to the membrane through a phosphatidylinositol linkage. It shares some homology to 2 other EPH receptor ligands, B61 and LERK-2. The Elf-1 protein modulates proliferation, differentiation and survival of EPH receptor-expressing cells by stimulating or antagonising intracellular signalling mediated by the EPH receptor. Typical of many potential applications are increasing survival of neuronal cells in culture (e.g. where intended for transplantation), also therapeutically in increase neuron survival ce.g. treatment of Alzheimer's or Parkinson's diseases), to prevent nervous system and lymphatic tumours, to induce differentiation of hepatocytes to form an artificial liver, to induce cartilage and bone
                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                        338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                                                                                                                                                                            Gaps
     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reagent;
ic; therapeutic;
                                                                                                                                                                                                                                                                                                                              gagaggctacaccgtgcaggtgaacgtgaacgactatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggtgagcgctgtgggtgatggcggcggctataccgtggaggtgagcatcaacgactacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -cggggcgccgctgcccc
                                                                                                                                                                                                                                                                                                           42;
Nucleic acid encoding Elf-1 protein that binds to EPH-type - for production of Elf-1 protein, useful for regulating proliferation, differentiation, and survival of cells
                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                               Sequence 1809 BP; 342 A; 590 C; 504 G; 373 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccacgccggccacgagtactactacatctccacgcccactcacaacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          culture;
                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                         134;
                                                                                                                                                                                                                                                                                Score 139.6; DB 1
Pred. No. 9.7e-19;
; Mismatches 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ell surface receptors; of injury; delivery agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA;
                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                 8.0%;
larity 62.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                               53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LERK-6; hek; elk; cell
neurons; disorder; inju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                            1 Similarity
292; Conser
                                               2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-0CT-1996
                                                                                                                                                                                                                         formation
                                                                                                                                                                                                                                                                                 Ouery Match
Best Local S
Matches 292
                                                                                                                                                                                                                                                                                                                                                                                                                        gc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT14010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT14010
                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LERK-6
                                                                                                                                                                                                                                                                                                                                                     279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                               399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340
                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT14
õ
                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                             òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΩX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

ä

for

.rng

XX PN

```
125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                               The LERK-6 polypeptide encoded by this sequence can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by contact with the polypeptide.
                                                                                                                                                                                                                                                                                                 to hek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                           p
                                                                                                                                                                                                                                                                                              which binds delivery an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acaacagctcgggggtgggcccgggggcgggggccgggaggcggggcaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ggggcgccgctgccgccgagcgcatgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tcaagcgctgggagtgcaaccggccgcacgcacagccccatcaagttctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 other;
                                                                               LERK-6 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 17;
                                                                                                                                                                                                                                                                                             designated LERK-6 - useful for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 135.4;
Pred. No. 4.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
[<del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
Ö
                                             Location/Qualifiers
2..313
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; 104
                                                                                                                                                                                                                                                                                                                                           44pp; English.
                                                                                                                                                                                                                                                                                             g cytokine
receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
0
                                                                                                                                                    95WO-US12779
                                                                                                                                                                          95US-0538709
94US-0318393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.8%;
larity 70.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; 108
                                                                                /product=
                                                                                                                                                                                                                                                                                             encoding
surface r
                                                                                                                                                                                                                                                                                                                   screening procedures.
                                                                                                                                                                                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                          1996-209575/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
219; Conser
                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 BP;
                                                                                                                                                                                                                                                                     P-PSDB; AAR91284
                                                                                                                                                                                                             IMMUNEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actacatct
                                                                                                                                                                                                                                                                                            Isolated DNA
                      sapiens
                                                                                                     WO9610911-A1
                                                                                                                                                                         03-OCT-1995;
05-OCT-1994;
                                                                                                                                                                                                                                                                                                         cell
                                                                                                                                                                                                                                    Cerretti DP;
                                                                                                                           18-APR-1996
                                                                                                                                                   04-0CT-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local S
Matches 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                             (IMMI)
                                                                                                                                                                                                                                                                                                          elk
                      Homo
                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
                                            Key
                                                                                                                                                                                                                                                                                                         and
SS
```

```
The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the hek or elk receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the exceptor. The present sequence represents a expansion expansion from human reper.
                                                                                                                                injury;
disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gagagggctacaccgtgcaggtgaacgtgaacgactatctggatatttactgcccgcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcaagcgctgggagtgcaaccggcacgcccgcacagccccatcaagttctcggaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcgggggctacacggtggaggtgagcatcaatgactacctggacatctactgcccgcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --gggggcgccgccggccgagcgcatggagcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
66;
66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 135.4; DB Pred. No. 4.4e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
               ВР
              314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 108 C; 104 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
               mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 24; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence from human LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                     New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                   of human LERK-6
                                                                                                                                                                                                                                                                                                       97US-0920440
                                                                                                                                                                                                                                                                           98WO-US17772
               t
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%;
llarity 70.9%;
Conservative
                                                                       (first entry)
              CDNA
                                                                                                                                                                                                                                                                                                                                    IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-243567/20
P-PSDB; AAY06821.
              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity
219; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 314 BP;
                                                                                                    sednence
                                                                                                                                                                                                                 W09910495-A1.
                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                              04-MAR-1999.
                                                                                                                                                                                                                                                                                                      29-AUG-1997;
                                                                                                                                                                                                                                                                          27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                Cerretti DP;
                                                                       24-JUN-1999
             AAX32766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                    ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                    (IMMV
                                                                                                    Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
AAX32766
                                                                                                                            XEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

2;

g

g

qq

ò

à

ò

ä

12

RESULT

306

ογ

d

ò

```
243
                          임
                                                                     d
                                                                                                                                                                                                                                 XX
                                                ò
                                                                                                               g
                                                                                                                                    ò
                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A fragment of murine Lerk-6 DNA was isolated by PCR for use as a probe for a human Lerk-6 homologue. The probe however led to the identification of a human Lerk-7 gene (see AAT32699). The Lerk-7 gene and protein can be used for studying the role of Lerk-7 in conjunction with elk, hek and eck receptors. They can also be used for delivering diagnostic or therapeutic agents to cells, e.g. cancer cells. The Lerk-7 proteins can also exhibit neuroprotective or neurotrophic properties and can be used to treat neural tissue disorders.
                         419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 ulture; reagent;
diagnostic; therapeutic;
186 tcaagcgctgggagtgcaaccggcccgcggcgcccggggggccgctcaagttctcggaga
                    cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surf
to c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - which binds to cell
for delivering agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 555 BP; 102 A; 191 C; 151 G; 111 T; 0 other;
                                                                                                                                                                                                                                 culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 128.8; DB 17
Pred. No. 1.1e-16;
); Mismatches 82;
                                                                                                                                                                                                                            hek; elk; cell surface receptor; c
disorder; injury; delivery agent;
probe; cytokine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human Lerk-7 cytokine receptors elk, hek and eck, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 34; 49pp; English.
                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                           555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eceptors elk, hek and eck, us or treating neural disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.48;
illarity 67.78;
Conservative
                                                                                                                                                                                                                                                                                                                                                            95US-0396946
94US-0351025
                                                                                                                                                                                                                                                                                                                                       95WO-US15781
                                                                                                                                                                                    (first entry)
                                                                                                                                           CDNA;
                                                                                                                                                                                                           sednence
                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-287171/29
P-PSDB; AAW02587.
                                                                 428
                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
222; Conserv
                                                                actacatct
                                                                                                                                                                                                      Lerk-6 coding
                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                           WO9617925-A1
                                                                                                                                                                                                                                                                                                                                     05-DEC-1995;
                                                                                                                                                                                   28-NOV-1996
                                                                                                                                                                                                                                                                                                                 13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                           01-MAR-1995
06-DEC-1994
                                                                                                                                        AAT32700
                                                                                                                                                                                                                                                                                                                                                                                                                 Cerretti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 222
                                                                                                                                                                                                                            Lerk-6;
neuron;
                                                                                                                                                                                                                                                  Lerk-7;
                                          246
                                                               420
                                                                                    306
                                                                                                                             AAT327
                                                                                                                                                               Op
                                                               Q
                                                                                    d
```

```
238
                                                        298
                                                                         419
                                                                                                                                                                                                                                                   ell surface receptors; culture; reagent; injury; delivery agent; diagnostic; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The LERK-6 polypeptide encoded by this sequence can be used to isolate cells expressing hek/elk cell surface receptors, or to measure the biological activity of such receptors. The protein may also be used as a delivery agent, taking diagnostic and therapeutic agents to cells expressing such receptors. LERK-6 can also be used as a tissue culture reagent to enhance the viability or prolong the lifespan of the neurons. Neural tissue disorders and injuries may be treated by contact with the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hek
ţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine designated LERK-6 which binds treceptors - useful for drug delivery and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111
                                                                                                                               386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
G;
                                                                                                            447
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..555
                                                                                                                   actacatctccacgcccactcacaacct
                                                                                                                                                                                                                                                                                                                                    LERK-6
                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 33; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ċ;
                                                                                                                                                                           555
                                                                                                                                                                                                                                                                                                                                                                                                           95US-0538709
94US-0318393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 191
                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                 1..555
/*tag= a
/product=
                                                                                                                                                                           CDNA;
                                                                                                                                                                                                                                 coding sequence.
                                                                                                                                                                                                                                                  cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding and elk cell surface r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening procedures
                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                 hek; elk; c; disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-209575/21
                                                                                                                                                                          AAT14009 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV) IMMUNEX
                                                                                                                                                                                                                                                                                       musculus
                                                                                                                                                                                                                                                                                                                                                     WO9610911-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cerretti DP;
                                                                                                                                                                                                              10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-1995
05-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                       18-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                         04-OCT-1995
                                                                                                                                                                                           AAT14009
                                                                                                                                                                                                                                                            neurons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                  LERK-6;
                                                                                                                                                                                                                                LERK-6
                 179
                                   300
                                                     239
                                                                        360
                                                                                        299
                                                                                                           420
                                                                                                                                                                                                                                                                                       Mus
                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                 AAT14009
                                                                                                                                                                                                                                                                      SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
```

Length

128.8; DB 17; No. 1.1e-16;

Score Pred.

7.48;

Match Local Similarity

Query Best I

242

cagt

cact 182

cact

80

Db

ð

183

Q

acaacagetegggggtggggccegggggcceggaggegggggagg

ø

140

qq

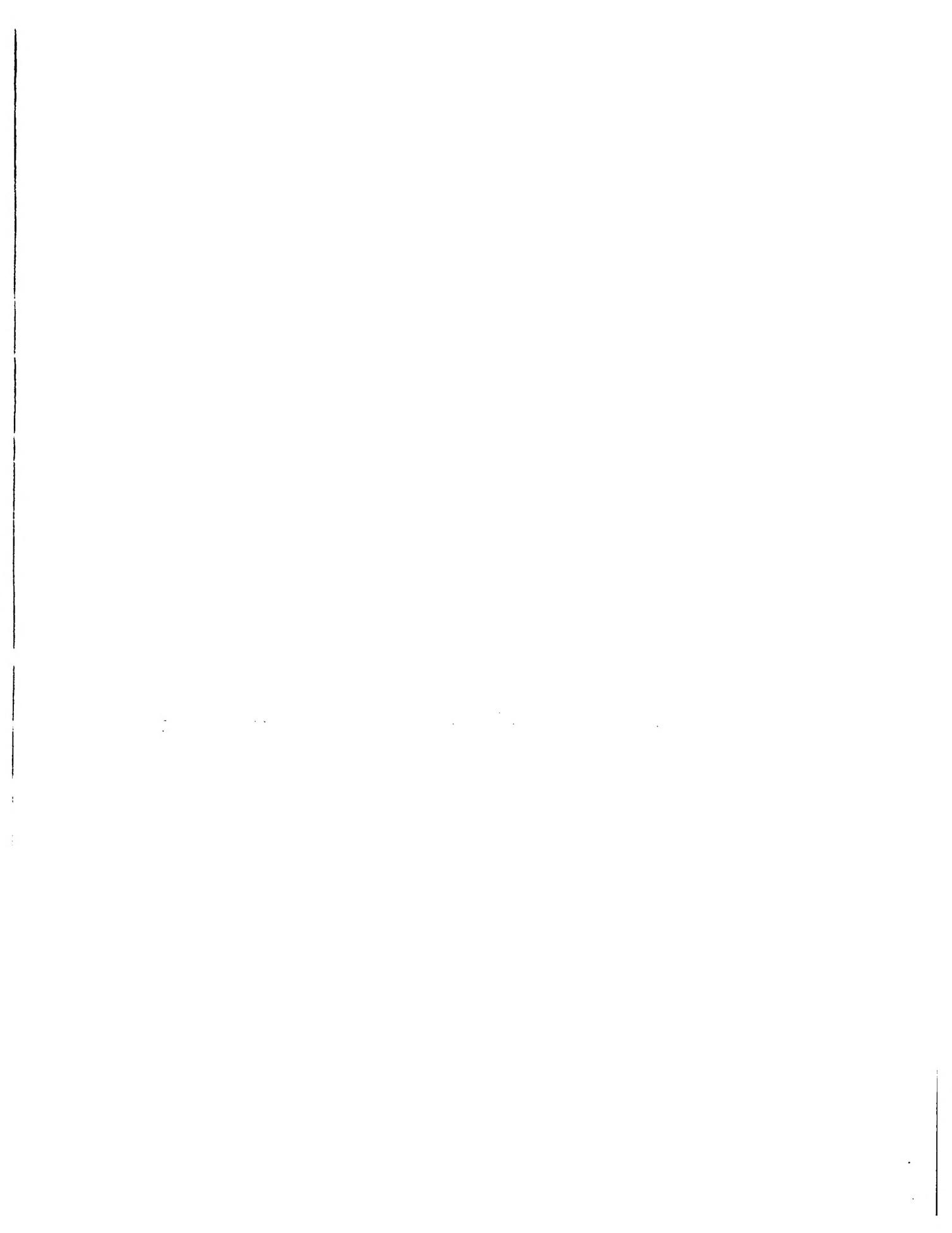
178

cggt

-cggggcgccgctgccccggctgagcgcatggag

```
<u>``</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates murine and human LERK-6 polypeptides that bind to hek/elk receptors. Host cells transfected or transformed with vectors comprising the LERK-6 nucleic acid sequences are used for the recombinant production of the proteins. LERK-6 polypeptides may be useful in the enhancement, stimulation, proliferation or growth of cells expressing the hek or elk receptor. The ligand and receptor complex may be involved in neural growth, development and/or maintenance. LERK-6 can be used for treating disorders of neural tissue such as injury or neurological diseases, either chronic or acute. LERK-6 may be employed in treating neurodegenerative conditions where there is neural death, excitotoxicity. In addition, they may be administered to a mammal to exert a trophic
                                                                                                                                                                                                                                                                                                                                                                                                           injury;
disease;
                                                                                                                                                                                                  gagtact 419
|| ||||||
gaatact 358
                     178
                                                                                                               299
                                                                                                                                    238
                                                                                                                                                         359
                                                                                                                                                                              298
    Gaps
                                                                cagaga
                                                                                                                                                           cggaga
                                                                                                                                                                                                                                                                                                                                                                                                       LERK-6 polypeptide; hek receptor; elk receptor; human; murine; cell proliferation; neural growth; neural tissue; neurological neurodegenerative; excitotoxicity; ss.
                                                                                                                                                     82;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Murine LERK-6 polypeptide encoding cDNA
                                                                                                                                                                                                                                            447
                                                                                                                                                                                                                                                    actacatctctgccacacctcccaacct 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46pp; English.
                                                                                                                                                                                                                                            actacatctccacgcccactcacaacct
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New cytokine designated LERK-6
                                                                                                                                                                                                                                                                                                                     555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0920440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US17772
                                                                                                                                                                                                                                                                                                                                                               (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                    AAX32761 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 37-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-243567/20
P-PSDB; AAY06820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9910495-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerretti DP;
                                                                                                                                                                                                                                                                                                                                                              24 - JUN-1999
222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04 - MAR - 1999
                                                                183
                                                                                      140
                                                                                                                                                                                                                    299
                                                                                                           243
                                                                                                                                                     300
 Matches
                                                                                                                               179
                                                                                                                                                                          239
                                                                                                                                                                                               360
                                                                                                                                                                                                                                                               359
                                                                                                                                                                                                                                         420
                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus
                                           g
                                                                                      a
                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                d
                                                                                                                                                                          ag
                                                                                                           à
                                                                                                                                                      ŏ
                                                                                                                                                                                                                    ga
                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                ò
                                                                                                                                                                                                                                         ò
```

```
3
effect on neural tissue. They can also be used as reagents for those conducting quality assurance studies e.g. to monitor shelf life and stability of elk protein under different conditions. The polypeptides can also be used as carriers for delivering agents attached to cells bearing the elk or hek cell surface receptor. The present sequence represents a cDNA encoding a murine LERK-6 polypeptide.
                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                              419
                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                       238
                                                                                                                                                      Gaps
                                                                                                                                                                           acaacagctcgggggtgggcccgggggcggggccggaggcggggcagagcagt
                                                                                                                                                                                                                                                                           ----cgggggcgccgctgccccggctgagcgcatggagcggt
                                                                                                                                                                                                                                                                                                                                                                              agttccagcgctacagcgccttctctgggctacgagttccacgccggccacgagtact
                                                                                                                                                                                                                                                                                                                                                                                                      299 agttecaactetteacecettttecetgggetttgagtteeggeetggeeacgaataet
                                                                                                                                                    24;
                                                                                                                             Length
                                                                                                                                                     Indels
                                                                                        T; 0 other
                                                                                                                             DB 20;
                                                                                                                          Score 128.8; DB 20 Pred. No. 1.1e-16; ); Mismatches 82;
                                                                                        G; 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                                                                                                                                                              447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09:53:34
                                                                                      Sequence 555 BP; 102 A; 191 C; 151
                                                                                                                                                                                                                                                                                                                                                                                                                              actacatctccacgcccactcacaacct
                                                                                                                                                    .;
0
                                                                                                                           ch 7.4%;
11 Similarity 67.7%;
222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 13,
Job time: 4204 sec
                                                                                                                           Query Match
Best Local S
Matches 222
                                                                                                                                                                                                                                                      Ġ
                                                                                                                                                                                                    80
                                                                                                                                                                                                                            183
                                                                                                                                                                             123
                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                              420
                                                                                                                                                                                                                                                                                                                                                                                                                                                       359
888888888
                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                              Qγ
```



```
cell updates/sec
                                                                                                                                                                                                                                                                   aaaaa 1743
                                                                                                                              Search time 2227.85 Seconds (without alignments) 16372.266 Million cell up
                                                                                                                                                                                                                                                                    .... ааааааааааааааа
                                                                                                                                                                                                                                                                                                                                                                                                                        3595312
4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                              residues
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
 version -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
                                                                                                                                  ••
                                                                                                                                                                                                                                                                                                                                                                          1797656 seqs, 10463268293
                                                                                                                                                                                                                 US-09-733-756-1
1743
1 gctgctgctgctgctgc..
                                                                                                                             2002, 08:42:05
                                                                                                                                                                                                                                                                                                                                1.0
 GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                Gapext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenEmbl:*

1: gb_ba:*
2: gb_htg:*
3: gb_om:*
5: gb_ow:*
6: gb_ph:*
7: gb_ph:*
3: gb_pl:*
1: gb_pl:*
3: gb_vi:*
6: gb_vi:*
6: gb_vi:*
7: gb_ph:*
7: gb_ph:*
8: gb_vi:*
8: gb_vi:*
6: gb_vi:*
6: gb_pi:*
7: gb_pi:*
7: gb_pi:*
8: gb_vi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 ,
                  Copyright
                                                                                                                              July 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq
                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                           score:
                                                                                 OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
DB
                                                                                                                                                                                                                 Title:
Perfect sc
Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum
Maximum
                                                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Query
No. Score Match Length DB ID

23.6 8 96.3 1769 9 BC017722 23.8 64.5 178826 2 ACC01890 24.9 52.7 1037 6 AR0040292 17.8 52.7 1037 6 AR0040871 17.8 52.7 1037 6 AR014632 25.3 14.5 18.8 5 AR014632 25.3 14.5 18.8 5 AR12404 22. 12.2 16.9 18.9 6 AR023764 24.1 10.5 186 6 AR322137 25.2 12.7 2 25.3 10 AV04557 25.2 12.7 18 6 642 6 AR122044 29.2 8.6 642 6 AR134682 29.6 8.0 1540 10 AM014742 29.6 8.6 186 9 HSGMC02 25.4 7.8 36.95 9 ACC04258 25.5 14.8 0 1899 6 AR13466 25.6 8.0 1540 10 AM014752 25.7 1480 6 AR033764 25.8 6.7 649 10 AR130336 25.4 7.8 36.95 9 ACC043818 25.4 7.8 36.95 9 ACC043818 25.4 7.8 36.95 9 ACC04388 25.4 7.4 6.7 1480 6 AR04374 25.5 6 AR13467 26.8 18.8 10 ACC04388 26.8 6 7 1480 6 A	017722 Homo 021890 Homo 004292 Sequ 001064 Sequ 080871 Sequ	809 Sequence 1 187 Human recep 360 Homo sapien 04632 Mus muscu 04327 Mus muscu 51678 Danio rer	2885 Mus musc 2885 Mus musc 32137 Sequenc 39777 Ctenoph 34683 Sequenc 52044 Sequenc 332 Gallus ga 23765 Sequenc 07292 Homo sa 1941 Mus musc 1752 Mus musc	TO A CO	RNA linear PRI 06-DEC-2001 1335 IMAGE:4397263, mRNA, ta; Vertebrata; Euteleostomi; hin1; Hominidae; Homo. titutes of Health, Mammalian cs Office, National Cancer 03, Bethesda, MD 20892-2590, nih.gov
23.8 96.3 17.8 17.8 17.8 17.8 17.8 17.8 17.8 17.8	BC01772 AC02189 AR00429 AR08087 AR16446	120809 HSU14187 HUMEFL2 AC104632 AC104327 AB051678	AX332137 AF209777 AF209777 AR134683 AR152044 CHKELF1L AR023765 HSA7292 MMU1494 OMU1475 AR023764	AR134 682 AR152043 HS6LK02 AC004258 GDRNARAG AR134677 AR134677 AR152038 DRTKRAL1 AC073818 XLU31204 XLU31204 XLU31205 DRTKLELF MMU90666 AF317286 AF317286 AF317286 AF317286 AR103236 IS6902 IS6902 IS6902	ALIGNMENTS 1769 bp m -A3, clone MGC:2 Chordata; Crania Primates; Catarr 01) National Ins), Cancer Genomio Drive, Room 11A http://mgc.ncisk .nih.gov
10	6.3 17582 4.5 17582 4.5 107 2.7 103 2.7 103	2.6 103 2.6 98 0.4 75 6.9 28957 6.8 32675 4.5 183	22.7 20.5 20.5 20.5 20.5 20.0 20.0 20.0 20.0	8 3629 8 3629 8 3629 9 16236 9 16236 1 1655 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	sapiens, lete cds. 7722 7722 7722.1 GI 7722.1 GI sapiens ryota; Met alia; Euth bases 1 to usberg, R. ct Submiss itted (03-1 Collection itute, 31 (
Hubi design E	1678 1123 949 917 917	917, 9 91, 10 643, 11 642, 12 25, 13 241,	14 22 16 183. 17 149. 20 149. 22 139. 24 139.	25 26 27 28 29 29 31 32 33 33 33 34 34 35 36 37 37 39 39 30 41 42 41 41 42 43 44 41 45 46 47 47 48 48 48 48 48 48 48 48 48 48	

```
Ö
                   Genome
CA 943
                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
                                                                                                                                                                                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480
                                                  ΜŊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                          9
                                                                          n can be
                                                   nd
                                                                                                                                                                                                                                                                                                                          33355
11111
333333
                                                                                                                                                                                                                                                                                                                                                        ctgcg
||||||
                                                                                                                                                                                                                                                                                                                                                                                        cgca
||||||
                                                                                                                                                                                                                                                                                                                                                                                                                       LNL)
luman
ord,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gett
|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tca
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Sequencing Group at the Stanford Hum
Center, Stanford University School of Medicine, Stanfor
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A.,
                                                                                                                                                                                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information through the I.M.A.G.E. Consortium/LLNL at: http://imagSeries: IRAK Plate: 27 Row: d Column: 19.
Location/Qualifiers
1. .1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ctgctgcgcctccacatcgcactccgggggagaagccggtccccactctccccagt
                                                                                                                                                                                                                                                                                           17
                                                                                                                                                                                                                                                                                           Length
                                                                                                            /organism="Homo sapiens"
/db_xref="LocusID:1944"
/db_xref="LocusID:1944"
/db_xref="taxon:9606"
/clone="MGC:21335 IMAGE:4397263"
/tissue_type="Duodenum, adenocarcinoma"
/clone_lib="NIH_MGC_88"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
/1. .787
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                          Score 1678.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                         96.3%;
ilarity 99.9%;
Conservative
                                                                                                                                                                                                                                                                                                 Local Similarity
Les 1680; Conser
                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 1680
                                                                                                                                                                                                                                                           COUNT
                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                     205
                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                   265
                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                               FEATURES
                                                                                                                                                                                                                                                          BASE CC
ORIGIN
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D
D
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
1104
                                                                                       0
                                                                                                 0
                                                                                                          200
                                                                                                                84
                                                                                                                     0
                                                                                                                              20
                                                                                                                                        80
                                                                                                                                             464
                                                                                                                                                            500
                                                                                                                                                                                1620
                           20
                 9
                                     80
                                               840
                                                         00
                                                                   9
                                                                                                                                                                           マ
                                          64
                                                    924
                                                                                       08
                                                                                                                                                                 58
                                                                                                                                                                           64
                                                                                                     \sim
  9
       ga
                                              agcctagtgggcctagacccctccccatggctagaagtggggcctgcaccatacatct
                                                         000
                                                                                                                    gaaccatctcccaggaccttgccctgctcaccctatgtggtcccacctatcctcctg
                                                                                      GGGAGAAGCCGGTCCCCACT
CATCGCACTCCG
       cgg
                                                                                                           g
                                                                                                               Ū
                 601
                                745
                                     721
                                          805
                                                   865
                      5
                           61
                                               81
                                                         841
                                                                   901
                                                                        S
                                                                            961
                                                                                 S
                                                                                      1021
                                                                                                1081
                                                                                                     1165
                                                                                                          1141
                                                                                                               1225
                                                                                                                              261
                                                                                                                                             1405
                                                                                                                    201
                                                                                                                                        321
                                                                                                                                                       65
                      68
                                                                                                                                                            441
                                                                                                                                                                 5
                                                                                                                                                                      501
                                                                                                                                                                           585
  99
                                                                                                                                                                                561
                                                                                  104
                                                                                           110
                                                              92
                                                                        98
                                                                                                                                                                 52
                                                                                                                         28
                                                                                                                                   34
            q
       δ
                     a
                                qq
                                               οχ
                                                   qq
                                                              ga
                 õ
                           ò
                                     ô
                                          a
                                                                        q
                                                                                                ŏ
                                                         ò
                                                                   ò
                                                                                 g
                                                                             ò
                                                                                      ò
                                                                                           a
                                                                                                     a
                                                                                                                         d
                                                                                                          ò
                                                                                                               a
                                                                                                                    ò
                                                                                                                              ò
                                                                                                                                   g
                                                                                                                                             g
                                                                                                                                        ò
                                                                                                                                                       g
                                                                                                                                                                 d
                                                                                                                                                  ò
                                                                                                                                                            ò
```

Tue

RESULT

d

ŏ

dd

ò

SOURCE

```
Loca
            Center:
Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21032
21132
40476
40576
57618
57718
75709
75809
89019
89119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100449
110705
110805
123157
123257
132468
141562
146677
151202
151202
155823
160149
160149
160249
1633125
168114
169868
171681
171581
172883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                    humon saplens
Eukaryota, Wetazoa; Chorddta; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Wetazoa; Chorddta; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 175826)
I (bases 2 to 175826)
I (bases 2 to 175826)
I (bases 3 to 175826)
I (bases 4 to 175826)
I (bases 5 to 175826)
I (bases 6 to 175826)
I (bases 7 to 175826)
I (bases 8 to 175826)
                                                                                                                                                                                                                                                       HTG 10-NOV-2000
DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One
CGGGAACCATCTCCCAGGACCTTGCCCTGCTCACCTATGTGGTCCCACCTATCCTCCTG 1704
                                     Worley, K.C.
Worley, K.C.
Direct Submission
Submitted (22-JAN-2000) Human Genome Sequencing Center, Deparsof Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2000 this sequence version replaced gi:9719697.
                                                                                                                                                                                                                                     175826 bp DNA linear
chromosome 3 clone RP11-498A2, WORKING
pieces.
                                                                                                                                                                                                                                            AC021890
Homo sapiens chromosome 3 clone
22 unordered pieces.
AC021890
AC021890.12 GI:11128300
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                  1681 aa 1682
                                                                                                                                                     1765 AA 1766
                                                                                                                                                                                                                                                 LOCUS
DEFINITION
                                                                                                                                                                                                               \sim
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
  1645
                                                                          1705
                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                       1621
                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                AC021890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
```

TITLE

TITLE

COMMENT

```
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                      Center clone name: RP11-498A2

Center clone name: RP11-498A2

Sequencing vector: M13; L08821

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 144734 bases at least Q40

Consensus quality: 162873 bases at least Q30

Consensus quality: 169424 bases at least Q20

Estimated insert size: 170770; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 3.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f unknown length
g of 11230 bp in length
f unknown length
g of 10256 bp in length
f unknown length
g of 12352 bp in length
f unknown length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                   f unknown length of 19344 bp in length f unknown length of 17042 bp in length f unknown length of 17991 bp in length f unknown length of 13210 bp in length f unknown length f unknown length
                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length length bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     фq
of Medicine
                                                                                                                                                                                                                                                                                                                                                           21031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 8894 |
unknown
of 5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 4525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
of 2776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 4326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1654
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 1449
unknown
of 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 2215
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 4421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                          of
                                                               HMZE
                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ation/Qualifiers
.175826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                            Center project name:
                                                                                                                                                                                                                                                                                                                                                       21031:
21131:
40475:
40575:
57617:
57717:
75708:
89018:
89118:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110704:
110804:
123256:
123256:
132467:
141461:
141561:
146576:
151201:
151201:
15322:
160248:
163024:
163124:
163124:
168113:
169867:
169967:
            BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100448:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171680:
 : Baylor
code: B(
                                                                                                                                                                                                                                                                                                                                  as soon as i
```

р

```
ö
                                                                                  39217
                                                                                                                                                         39457
                                                                                                    39277
                                                                                                                                                                           39517
                                                                                                                                                                                             39577
                                                                                                                                                                                                                                 39697
                                                                                                                                                                                                                                                                     39817
                                                                                                                      3933
                                                                                                                                       39397
                                                                                                                                                                                                               39637
                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                         39937
                                                                                                                                                                                                                                                                                                                           39997
                                                                                                                                                                                    1051
                                                                                                                                                                                                                       1171
                                                                                                                                                                                                      1111
                                                                                                                                                                                                                                          1231
                                                                                                                                                                                                                                                            1291
                                                                                                                                                                                                                                                                              1351
                                                                                                                                                                                                                                                                                       3987
                                                                                                                                                                                                                                                                                                                  1471
                                                        631
                                                                 391
                                                                         691
                                                                                           51
                                                                                                             811
                                                                                                                                                                                                                                                                                                                                    1531
                                                                                                                                                 931
                                                                                                                                                                   991
                                                                                                                                                                                                                                                  397
                                               Gàps
                                                                       agccccaaacgggaacacctgccctggccgtgggcatcgccttcttcctcatgacgttc
                                                                                           gaagg
||||||
                                                     ccatg
||||||
                                                                                                                                                                                    catat
[[]]]
catat
                                                                                                                             gggca
||||||||
|GGGCA
                                                                                                                                                                ggatt
||||||
GGATT
                                                                                                                                                                                                                                                                             tgtac
||||||
|GTAC
                                                                                                                                                                                                                        ccctg
                                                                                                                                                                                                                                CCCTG
                                                                                                                                                                                                                                                          Saget
                                                                                                                                                                                                                                                                                                         AGCT
                                                                                                                                                                                                                                                                                                                  tctt
                                                                                                                                                                                                                                                                                                                                     aaca
                                      58
                                               .;
0
                                                                                         ttgtcttctgtgaagacaggacctatgcaacgcacagacacttttggagaccgtaa
                                                                                                                                                                                  gcccccagagagagaaatcgaagcgtgggaggcaccccattgctctcctccag
                                                                                                                                                                                                                     _
                                      th
                   other
                                              Indels
                                      Leng
                   33
                                    DB 2;
208;
2;
                   21
                                          ė,
                   ļ
                                    Score 1123.8;
Pred. No. 7.7e
0; Mismatches
                   3
                   4
 ap
60
              29
              98A
/organism="Homo s/db_xref="taxon:
/chromosome="3"
/clone="RP11-4981a 46653 c 47059
      ••
                                            0;
                                    64.5%;
ity 99.8%;
servative
                  ď
                                    Query Match
Best Local Similari
Matches 1125; Cons
                  38
                  \boldsymbol{\sigma}
                  BASE COUNT
ORIGIN
                                                      3
                                                                                39158
                                                                                         692
                                                                                                                    9278
                                                                                                  218
                                                                                                           52
                                                                                                                            812
                                                                                                                                      9338
                                                              39098
                                                                                                                                                                32
                                                                                                                                              872
                                                                                                                                                                         9458
                                                                                                                                                                                  992
                                                                                                                                                                                                    1052
                                                                                                                                                                                                             9226
                                                                                                                                                       9398
                                                                                                                                                                                           518
                                                                                                                                                                                                                               8696
                                                                                                                                                                                                                                       1172
                                                                                                                                                                                                                                                 8696
                                                                                                                                                                                                                                                          1232
                                                                                                                                                                                                                                                                  9758
                                                                                                                                                                                                                                                                            1292
                                                                                                                                                                                                                                                                                     39818
                                                                                                                                                                                                                                                                                              ^{\circ}
                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                               1412
                                                                                                                                                                                                                                                                                                                        9938
                                                                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                                                                              135
                                                                                                                                                                                                                                                                                                       3987
                                                                                                                                                                                                                                                                                                                                 147
                                                                                                           ~
                                                                                                                                                                φ
                                                              qq
                                                                                a
                                                                                                  g
                                                                       δ
                                                                                                                    d
                                                                                                                                      a
                                                                                         ð
                                                                                                                                                                         ga
                                                                                                           ŏ
                                                                                                                             ò
                                                                                                                                                                                           g
                                                                                                                                               ò
                                                                                                                                                                ò
                                                                                                                                                                                                             g
                                                                                                                                                                                  δ
                                                                                                                                                                                                    ò
                                                                                                                                                                                                                               a
                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                        φ
                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                           ò
```

Q

õ

Q

```
-DEC-19
                                                              40177
                                                                                                                                                                                      Σ
                                                                                                                                                                                      Goldfarb,
                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                           239
                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                      287
                                                                                                                                                                                                                                                                                                                                                                                                                 347
                                                                                                                                                                                                                                                                                                                                                                                                                               360
                                                                                                                                                                                                                                                                                                                                                                                                                                             407
                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527
                                                                                                                                                                                                                                                                                         9
04
                                                                                                                                                                                                                                                                                       getgetgetgetgetgetcgtgecegtgecgetgetgecgetgetgecgggeceaagggee
                                                                                                                                                                                                                                                                                                                  cggagggggcgctgggaaaccggcatgcggtgtactggaacagctccaaccagcacctgcg
                                                                                                                                                                                                                                                                                                                                             gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt
                                                                                                                                                                                                  family
                                                                                                                          PAT
                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                               1070
                                                                                                                                                                                     Maisonpierre, P.C.,
                                                                                        40224
                                                                                                                                                                                                   Eph
                                                                         linear
                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                    other
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                  ^{\rm of}
                                                                                                                                                                                                                                    10
                                                                                                                                                                                                  activity
                                                                                                                                                                                                                                                            Score 949.2; DB 6;
Pred. No. 3.6e-174;
); Mismatches 18;
                                                                                                                                                    Unknown.

Unclassified.

Unclassified.

1 (bases 1 to 1070)

Davis,S., Gale,N.W., Aldrich,T.H., Mai
and Yancopoulos,G.D.
Method of enhancing the biological act
Patent: US 5747033-A 8 05-MAY-1998;
Location/Qualifiers
                                                                                                                                                                                                                                    į,
                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                    œ
                                                                                                                         1070 bp
US 574703
                                                                                                                                                                                                                   1. .1070
/organism="unknown"
341 c 334 g
                                                                                                                                                                                                                                                                          ;
                                                                                                                               from patent
                                                                                                                                            GI:3965171
                                                                                                                                                                                                                                                             54.5%;
illarity 97.0%;
Conservative
                                                                                                                       AR004292
Sequence 8
AR004292
AR004292.1
                                                                                                                                                                                                                                                                   Local Similarity
les 976; Conser
                                                                                                                                                                                                                                   ಥ
                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 976
                                                                                                         RESULT 3
AR004292
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                      source
                                                                                                                                                                ORGANISM
                    1532
                                 40058
                                                            40118
                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                   COUNT
      39998
                                              1592
                                                                         1652
                                                                                                                                                                                                       JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                    09
                                                                                      40178
                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                        _
                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                288
                                                                                                                                                                                                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468
                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                  BASE CO
                                                                                                                                                          SOURCE
                                 d
                                                            g
                    õ
                                              δ
                                                                          Qy
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
RESULT 5
AR080871
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
17
          181
                                                                397
                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                     277
                                           337
                                                     301
                                                                                     457
                                                                                                                                                                                                                                                                                                                                                                                          sourc
                                                                           361
                                                                                                                               577
                                                                                                                                                                                                                                                                                                                                                                                                    COUNT
                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                     81
                                                                                                                                            541
                                                                                                                                                      637
                                                                                                                                                                 601
                                                                                                                                                                            697
                                                                                                                                                                                      661
                                                                                                                                                                                                 757
                                                                                                                                                                                                            721
                                                                                                                                                                                                                      817
                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                            877
                                                                                                                                                                                                                                                                937
                                                                                                                                                                                                                                                                                      997
                                                                                                                                                                                                                                                                            901
                                                                                                                                                                                                                                                                                                                                                                                   EATURES
                                                                                                                                                                                                                                                                                                                                                                                                   ы
                                                                                                                                                                                                                                                                                                                                                                                                   BAS
          ò
                     a
                                          q
                                                                g
                                                                                     g
                                ò
                                                      õ
                                                                                                           ద
                                                                                                                                                                                                 qq
                                                                                                                                                                                                           Qγ
                                                                           ò
                                                                                                 ò
                                                                                                                     ò
                                                                                                                                                     g
                                                                                                                                                                           g
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                 g
                                                                                                                                           Q
                                                                                                                                                                 Q
                                                                                                                                                                                      Q
                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                      04-DEC-199
                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                      1007
    540
               587
                          009
                                    647
                                                099
                                                                      720
                                                                               767
                                                                                           780
                                                                                                               840
                                                          707
                                                                                                                                     900
                                                                                                                                                          960
                                                                                                     827
                                                                                                                          887
                                                                                                                                               947
                                                                                                                                                                                                                                                                                                                                                            156
                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                  9
    agttcac
|||||||||||
\GTTCAC
                          tcaggt
||||||
                                                sectage
|||||||
                                                                                           aaggga
|||||||
                                                                     tacatct
|||||||||
                                                                                                                                   999
                                                                                                                                                                     TGGGGG
                                                                                                                                                                                                                                                                                                                                                Seegea
                                                                                                                                                                                                                      PAT
                                                                                                                                                           tgg
                                                                                                                                                                                                                                                                                                                                       .;
0
   cgtgggcatcgccttcttcctcatgacgttcttggcctcctagctctgcccct
                                                                                         agcctagtgggcctagacccctcccatggctagaagtggggcctgcaccata
                                                                                                                                                         10.
                                                                                                                                                                                                                                                                                                                                                                                            gcgagagggctacaccgtgcaggtgaacgtgaacgactatctggatatttactg
                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                            hek
                                                                                                                                                                                           05
                                                                                                                                                                                                                                                                           eceptor
                                                                                                                                                                               Unknown.

Unclassified.

Unclassified.

1 (bases 1 to 1037)

3 Beckmann, M. Patricia. and Cerretti, D. P.

Cytokines that bind the cell surface rece

Cytokines that bind the cell surface rece

L Patent: US 5738844-A 1 14-APR-1998;

Location/Qualifiers

1. 1037

1. 1037

237 g 170 t
                                                                                                                                                                                                                                                                                                                          Score 917.8; DB 6
Pred. No. 4.4e-168
; Mismatches 2
                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                     1037 bp
US 5738844.
                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                          patent
                                                                                                                                                                                                                                     GI:3963131
                                                                                                                                                                                                                                                                                                                           ch 52.7%;
l Similarity 99.8%;
919; Conservative
                                                                                                                                                                                                                          from
                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                    AR001064
Sequence
AR001064
AR001064
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 919
                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                     RGANISM
                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
   81
                                   588
                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                         541
                                                        648
                                                                              708
                                                                                         721
                                                                                                   768
                                                                                                                                   841
                                                                                                                                                                                                                                                                              JOURNAL
FEATURES
                                              601
                                                                   661
                                                                                                              781
                                                                                                                        828
                                                                                                                                              888
                                                                                                                                                         901
                                                                                                                                                                    948
                                                                                                                                                                                          1008
                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                         RESULT
AR001064
LOCUS
              a
                                   g
                                                        d
                                                                              g
                         ò
                                                                                                                                              d
                                              ò
                                                                   ò
                                                                                         ò
                                                                                                  q
                                                                                                              ò
                                                                                                                        g
                                                                                                                                   ò
                                                                                                                                                         ò
                                                                                                                                                                    a
                                                                                                                                                                                         g
                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                g
```

```
-AUG-2000
          0
                     336
                                 300
                                                       9
                                                                  456
                                                                             420
                                                                                       516
                                                                                                  480
                                            9
                                                                                                                        540
                                                                                                                                   636
                                                                                                                                              009
                                                                                                                                                                    099
                                                                                                                                                                                          720
                                                                                                                                                                               56
                                                                                                                                                                                                     816
                                                                                                                                                                                                                780
                                                                                                                                                                                                                           876
                                                                                                                                                                                                                                      840
          gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                       GCGAGAGGGCTACACCGTGCAGGTGAACGTGAACGACTATCTGGATATTTACTGCCCGCA
                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                              Unknown.

Unclassified.

Unclassified.

( bases 1 to 1037)

Beckmann, M. Patricia and Cerretti, D. P. Antibodies that bind hek ligands

L Patent: US 5969110-A 1 19-OCT-1999;

Location/Qualifiers

1. 1037

/organism="unknown"

/organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                           Δ,
                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                        37 bp
596913
                                                                                                                                                                                                                                                                                                                        10
US
                                                                                                                                                                                                                                                                                            1017
                                                                                                                                                                                                                                                                                  921
                                                                                                                                                                                                                                                                                                                                         GI:10007600
                                                                                                                                                                                                                                                                                                                              patent
                                                                                                                                                                                                                                                                                  from
                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                       AR080871
Sequence
AR080871
AR080871.
```

.rg

_

56

-7 3 $\boldsymbol{\alpha}$ 7

σ 0

S

0

Gaps

ö

Indel

7

Ö

9

15

ctgcg |||||

180

cccgca |||||||

240

336

Igagca ||||||

300

Iggett |||||||| |GGCTT

396

360

456

gagaa |||||| |GAGAA

95-05 -05 -05 -05

420

cta

ta

516

TACTA

480

ttegt |||||| TTCGT

540

ttcac

636

ctccccagt ||||||||||||

009

969

caggt ||||||||| CAGGT

99

ctggc |||||| CTGGC

756

720

816

secetg ||||||

780

876

840

catct ||||||

936

900

1111

55555

9

SULT

-2001

```
ctgctgcgcctccacatcgcactccggggagaagccggtccccacta
  2 8 8
    9
  E E
  ė
 Score 91/.0,
Pred. No. 4.4e
0; Mismatches
       ö
                                                                                                                                                                   1017
                                                                                                                                                              921
,2.7%;
99.8%;
itive
                                                                                                                                                              tyer
    imilarit
; Conse
                                                                                                                                                    Query Match
Best Local Si
Matches 919;
                                    Ō
                97
                                   217
                     61
                          57
                               121
                                         181
                                             277
                                                  241
                                                       337
                                                            301
                                                                      361
                                                                 397
                                                                                    517
                                                                           457
                                                                               421
                                                                                         481
                                                                                              577
                                                                                                   541
                                                                                                        637
                                                                                                                 697
                                                                                                            601
                                                                                                                      661
                                                                                                                           757
                                                                                                                                721
                                                                                                                                     817
                                                                                                                                          81
                                                                                                                                               877
                                                                                                                                                        37
                                                                                                                                                             901
                                                                                                                                                                  97
                                                                                                                                                        ₫ h
                                                                                                                                                                  ð
                d
                          d
                                                            οy
                                                                 q
                     Q
                                    셤
                                             a
                                                                           g
                               ò
                                        ò
                                                  Ω
                                                       QQ
                                                                                    q
                                                                      ò
                                                                                ŏ
                                                                                         ά
                                                                                              a
                                                                                                       g
                                                                                                                 d
                                                                                                                      δ
                                                                                                   ò
                                                                                                            ò
                                                                                                                           a
                                                                                                                                     Ωp
                                                                                                                                οχ
                                                                                                                                                        g
                                                                                                                                                             ò
```

```
156
                                                                                                                                                                                             276
                                                                                                                                                                                                        240
                                                                                                                                                                                  0
                                                                                                                                                                                                                   336
                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                         396
                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                              456
                                                                                                                                                                                                                                                                          420
                                                                                                                                                                                                                                                                                                480
                                                                                                                                                                                                                                                                                                           576
                                                                                                                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                                                                 636
                                                                                                                                                                                                                                                                                                                                            009
                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                       969
                                                                                                                                                                                                                                                                                                                                                                  099
                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                         720
                                                                                                                                                                                                                                                                                                                                                                                                    816
                                                                                                                            Gaps
                                                                                                                                      9
                                                                                                                                                                                  18
                                                                                                                                     gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                                                                                                                                                                                   PAT
                                                                                                                           ö
                                                                                                                1037
                                                                                                                 Length
       linear
                                                                                                                           Indels
                                                                                                               core 917.8; DB 6
red. No. 4.4e-168
Mismatches 2
                            Unknown.

Unknown.

Unclassified.

1 (bases 1 to 1037)

Beckmann, M. Patricia and Cerretti, D. P.

Cytokines that bind the cell surface re

Cytokines that bind the Cell surface re

L Patent: US 6274117-A 1 14-AUG-2001;

Location/Qualifiers

1. 1037

/Organism="unknown"

/organism="unknown"
       DNA
       1037 bp
US 6274117
                                                                                                                Score
Pred
                                                                                                                          ;
                       509
            patent
                       GI:16237
                                                                                                               / Match 52.7%;
Local Similarity 99.8%;
nes 919; Conservative
            from
            П
                       ۲.
      AR164469
Sequence
AR164469
AR164469
AR164469
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                       ORGANISM
                                                                               sourc
                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                         BASE COUNT
ORIGIN
                                                                                                               Query Ma
Best Loc
Matches
                                                                                                                                                 97
                                                                                                                                                            61
                                                                                                                                                                       57
                                                                                                                                                                                            217
                                                                                                                                                                                 121
                                                                                                                                                                                                       181
                                                                                                                                                                                                                  277
                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                        337
                                                                                                                                                                                                                                                   301
                                                                                                                                                                                                                                                              397
                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                    457
                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                          517
                                                                                                                                                                                                                                                                                                                                577
                                                                                                                                                                                                                                                                                                                                                      637
                                                                                                                                                                                                                                                                                                                      481
                                                                                                                                                                                                                                                                                                                                            541
                                                                                                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                                                                                                            697
                                                                                                                                                                                                                                                                                                                                                                                        661
                                                                                                                                                                                                                                                                                                                                                                                                   757
                                                                         EATURES
                                  SOURCE
                                                                                                                                                 g
                                                                                                                                                            ò
                                                                                                                                                                       qq
                                                                                                                                                                                            g
                                                                                                                                                                                  á
                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                             á
                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                    q
                                                                                                                                      ò
                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                       Dβ
                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                         Ω
                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                        ò
```

80

ggggggagagatggggcggggcttggaaggagcagggagcctttggcctctccaaggga

ó

```
ó
                                                                                        07-0CT-199
      876
                840
                                   900
                          936
                                             966
                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                             396
                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                                                                456
                                                                                                                                                                                                                                                                                                                                             480
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                       9
               catacatct
ceptor
                                                                                                                                                                                                     ggctt
                                                                                                                                                                                                                        Igagaa
||||||
                                                                                                                                                                                                                                                                                 gttccagcgctacagcgcctt.cctctgggctacgagttccacgccggccacgagtacta
                                                                                                                                                                                                                                                                                                                                           PAT
                                                                                                                                                                                            ö
                                                                                                                                                                                  137;
                                                                                                                                                                                                                                                              caagegetgggagtgcaaceggcegeecegeacagececeateaagtteteg
               agcctagtgggcctagaccctcctccatggctagaagtggggcctgcaccat
                                                                                                                                         ř
                                                                                                                                                                                   10
                                                                                                                                        surface
                                                                                                                                                                                   Length
                                                                                                                                                                                            Indels
                                                                                                                          Score 917.8; DB 6;
Pred. No. 4.4e-168;
); Mismatches 2;
                                                                                       DNA
                                                                                       1037 bp
US 5516658
                                                     ;
0
                                                                                           1 from patent
                                                                                                     GI:1601164
                                                                                                                                                                                  / Match 52.7%;
Local Similarity 99.8%;
les 919; Conservative
                                                                                                                   Unknown.
Unclassified
                                                                                      120809
Sequence
120809
120809.1
                                                                                                               Unknown
                                                                                                                                                                                  Query Match
                                                                             ~
                                                                                           DEFINITION
                                                                                                                   ORGANISM
                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                             REFERENCE
AUTHORS
TITLE
                                  841
                                                              997
     817
              781
                        877
                                           937
                                                     901
                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                            JOURNAL
                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                           121
                                                                                                                                                                                                              97
                                                                                                                                                                                                                                                    217
                                                                                                                                                                                                                                                                        277
                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                           337
                                                                                                                                                                                                                                                                                                              397
                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                                                                                                           421
                                                                                                                                                                                                                                                                                                                                                    517
                                                                                                                                                FEATURES
                                                                                120809
LOCUS
                                                                                                               SOURCE
                                  ò
                                           g
              ò
                        a
                                                     ò
                                                              a
                                                                                                                                                                                                              g
                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                       á
                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                           ò
```

```
PRI 04-FEB-1995 mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .987
/gene="EPLG3"
58. .774
/gene="EPLG3"
/gene="EPLG3"
/note="membrane-bound protein;
glycosyl-phosphatidylinositol (GPI) anchored"
/codon_start=1
/product="LERK-3"
/protein_id="AAC50078.1"
/protein_id="AAC50078.1"
/db_xref="GI:642833"
/translation="MAAAPLLLLLLVPVPLLPLLAQGPGGALGNRHAVYWNSSNQHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elk: isolation
                                              900
                        636
                                                                                              999
                                                                                                                                            720
                                                                                                                                                                   816
                                                                                                                                                                                           780
                                                                                                                                                                                                                 876
                                                                                                                                                                                                                                        840
                                                                                                                                                                                                                                                               936
                                                                                                                                                                                                                                                                                       900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 987)
Kozlosky,C.J., Maraskovsky,E., McGrew,J.T., VandenBos,T., Tee
Lyman,S.D., Srinivasan,S., Fletcher,F.A., Gayle,R.B. III,
Cerretti,D.P. and Beckmann,M.P.
Ligands for the receptor tyrosine kinases hek and elk: isolat
cDNAs encoding a family of proteins
Oncogene 10 (2), 299-306 (1995)
95140419
Cerretti,D.P.
Direct Submission
Submitted (01-SEP-1994) Immunex Corp., 51 University St., Sea
catgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaaccctcaggt
                                                                                                                                         agcctagtgggcctagaccctccccatggctagaagtgggcctgcaccatacatct
                                                                                                                                                                                                                                                                                      987 bp mRNA linear PRI 04 kinase ligand LERK-3 (EPLG3) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapien/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   HSU14187
Human receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:642832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .987
                                                                                                                                                                                                                                                                                                                                                                                                                                                        U14187
U14187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                œ
                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                     577
                                             541
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sourc
                                                                                                                                          661
                                                                     637
                                                                                            601
                                                                                                                  697
                                                                                                                                                                                        721
                                                                                                                                                                                                               817
                                                                                                                                                                                                                                                             877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                 757
                                                                                                                                                                                                                                       781
                                                                                                                                                                                                                                                                                                            937
                                                                                                                                                                                                                                                                                                                                     901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                      841
                                                                                                                                                                                                                                                                                                                                                           997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                               RESULT
HSU14187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                       rocus
                     d
                                                                    qq
                                                                                                                  đ
                                             οy
                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                             q
                                                                                                                                          ò
                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                     Óγ
```

ns

```
LYMVSRNGYRTCNAS
YISTPTHNLHWKCLR
QVPKLEKSISGTSPK
                                                                                             ö
                                                                                                                                                  180
                                                                                                                                                                       240
                                                                                                                                       191
                                                                                                                                                                                            300
                                                                                                                                                                                                                  360
                                                                                                                                                            251
                                                                                                                                                                                  311
                                                                                                                                                                                                       371
                                                                                                                                                                                                                            431
                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                 491
                                                                                                                                                                                                                                                            480
                                                                                                                                                                                                                                                                                  540
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                       551
                                                                                                                                                                                                                                                                                                                             099
                                                                                                                                                                                                                                                                                                                 671
                                                                                                                                                                                                                                                                                                                                                  720
                                                                                                                                                                                                                                                                                                                                                                        780
                                                                                                                                                                                                                                                                                                                                                                                             840
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             791
                                                                                                                                                                                                                                                                                                                                                                                   851
                                                                                                       9
                                                                                                     ctacaacagctcgggggtgggccccgggggcgggaccgggaggcggggggaggcagaagcagagcagaagcagaagcagaagcagaagcagaagcagaagca
                                                                                                                                                                                                                                             ACTA
                                                                                                                                                                                          tcgt
                                                                                                                                                                                                                                                                      TCGT
                                                                                                                                                                                                                                       acta
                                                                                                                                                                                                                                                                                                                 AGGT
                                                                                                                                                                                                                                                                                                                                                                                  GGGA
                                                                                                                                                                                                                                                                                                                                                                                             atct
                                                                                                                                                                                                                                                                               ıggga
                                                                                                                                                                                                                                                                                                        agg
                                                                                                                                                                                                                                    RREGYTVQVNVNDYLDIYCPHYNSSGVGPGAGPGGGGAEQYVL)
QGFKRWECNRPHAPHSPIKFSEKFQRYSAFSLGYEFHAGHEYYY;
MKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQY
REHLPLAVGIAFFLMTFLAS"
58. .123
                                                                                                                                                                                                                                                                                                                                                                     agcctagtgggcctagacccctcctcccatggctagaagtggggcctgcaccatac
                                                                                  987
                                                                                             Indels
                                                                                  Length
                                                                                 re 916; DB 9; Leed. No. 9.8e-168; Mismatches 0;
                                                            15
                    58. .123
/gene="EPLG3"
/note="putative"
124. .771
/gene="EPLG3"
/note="putative"
/product="unnamed"
a 329 c 323 g
                                                                                 Score; Pred.
                                                                             52.6%; Sc.
100.0%; P:
                                                                                            Conservative
                                                                                Match
Local Similarity
Hes 916; Conser
                                                            Ø
                                                           BASE COUNT
                                                                                                      Н
                                                                                                                           61
                                                                                                                                     132
                                                                                                                                                          192
                                                                                                                                                                     181
                                                                                                                2
                                                                                                                                                121
                                                                                                                                                                               252
                                                                                                                                                                                          241
                                                                                                                                                                                                     312
                                                                                                                                                                                                                          372
                                                                                                                                                                                                                                     361
                                                                                                                                                                                                                                                          421
                                                                                                                                                                                                                301
                                                                                                                                                                                                                                               432
                                                                                                                                                                                                                                                                     492
                                                                                                                                                                                                                                                                                          552
                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                     541
                                                                                                                                                                                                                                                                                                               612
                                                                                                                                                                                                                                                                                                                           601
                                                                                                                                                                                                                                                                                                                                     672
                                                                                                                                                                                                                                                                                                                                                661
                                                                                                                                                                                                                                                                                                                                                                     721
                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                Query
Best I
Matche
                                                                                                                                     q
                                                                                                                                                          a
                                                                                                                                                                               g
                                                                                                                                                ŏ
                                                                                                                                                                                                     g
                                                                                                                           9
                                                                                                                                                                                                                          g
                                                                                                                                                                     ò
                                                                                                                                                                                          ò
                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                a
```

```
PRI 09-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                      758 bp mRNA linear PRI 09-NOV-199
(clone hEHKl-L) EHKl receptor tyrosine kinase ligand
complete cds.
                                                                                                                                                                                               Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 758)

Davis,S., Gale,N.W., Aldrich,T.H., Maisonpierre,P.C., Lhotak,V.
Pawson,T., Goldfarb,M. and Yancopoulos,G.D.

Ligands for EPH-related receptor tyrosine kinases that require
membrane attachment or clustering for activity
Science (1994) In press
Location/Qualifiers
                    900
                                       971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                  gtgtccgcccctctaccccttcccccacgtagggcactgtagtggaccaagcacgggg
AGCCTAGTGGGCCTAGACCCCTCCTCCCATGGCTAGAAGTGGGGCCTGCACCATACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                 19. .723
/gene="EFL-2"
/function="binds EHK1 receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 704; DB 9; 1
Pred. No. 1.3e-126;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                     /cell_type="neuroblastoma"
1. 758
/gene="EFL-2"
19. 722
                                                                                                                                                                                                                                                                                                       1. ./ob
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hEHK1-L"
/cell_line="SH-SY5Y"
                                                                                                                                       Homo sapiens (clone hEHK1-L
(EFL-2) mRNA, complete cds.
L37360
L37360.1 GI:567003
ligand.
Homo sapiens cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.4%;
larity 98.4%;
Conservative
                                                          916
                                                         Similarity
                                                                                                                                HUMEFL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                     source
                                                                                                           6
                                                                                                                                        DEFINITION
                                                                             972
                                                                                                                                                                                                    ORGANISM
852
                                                          901
                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
                                     912
                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                 JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNT
                  841
                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                   HUMEFL2
                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE CO
                                                                                                           RESULT
                                                                                                                                LOCUS
                                     Оp
                                                                              ga
                  ò
                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
```

a

a

ò

ga

g

δ

g

õ

a

ò

g

ò

q

ò

Q

Q

```
preserved
                      2056
2156
4336
4336
6527
6527
6527
121443
121443
121207
121443
133924
435995
733333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
7333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
7333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73333
73
þe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-2001
DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siochemistry,
n 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi
Murinae; Mu
                                                                 320
                   300
                                                                                                                   360
                                                                                                                                                                                                                    420
                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         680
                                                                                                                                                                                                                                                                                                                                                                      500
                                                                                                                                                                                                                                                                                                                                                                                                                        540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                   ggagaa
|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                      gttcac
|||||||
|GTTCAC
              tcaggt
                                                                                                                                                                                                             gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                                                                                                                                                                                                                                               ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sceetg
||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC104632

AC104632

AC104632

AC104632

AC104632

AC104632.

AC104632.

AC104632.2

AC1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA linear HTG strain C57BL/6J, WORKING
                                                                                                            ctgctgcgcctccacatcgcactccggggagaagccggtccccactctccccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   er: Department Of Chemistry And Biochemistry
University Of Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Department
The University Of C
Center code: UOKNOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
AC104632/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                            321
                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                             381
                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                                                                                                                                                                                                              501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
JOURNAL
AUTHORS
TITLE
                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
```

length bp in length length bp in length length bp in length in length lt.
bp.
lengt.
rin l bp in length length bp in le length bp in le length bp in l length bp in l
length
bp in l ength th ength bp in length bp in length length bp in length op lengt. in th n le 7 bp . lengt. 7 in . th th ቲ ተ th th th length bp in l length bp in l th length length ength p in bp in \Box ni da lengt bp in eng eng leng eng eng eng dq len bp ф len bp len bp len bp unknown of 2191 unknown of 2085 unknown of 2761 unknown of 2817 unknown of 2080 unknown of 2828 unknown of 2488 unknown of 2034 unknown of 2145 unknown of 2162 unknown unknown of 2359 unknown of 1977 unknown unknown of 2323 unknown of 3005 unknown of 2038 unknown of 2105 unknown of 2557 unknown of 2301 unknown of 1988 of 2460 unknown of 2393 unknown of 2354 unknown of 3171 unknown of 1988 unknown of 2447 unknown of 3252 unknown of 3071 unknown of 2410 unknown unknown of 2105 unknown of 2439 unknown of 2460 unknown of 3180 unknown of 2367 unknown Jap of contig Jap of contig gap of gap of contig contig gap of contig gap of contig gap of contig contig gap of contig gap of contig gap of gap of contic gap of 2055: 4335: 4335: 66266: 121422: 121422: 141142: 16599: 73434: 73434: 73434: 733346: 733346: 733346: 733346: 73333346: 7333346: 7333346: 7333346: 7333346: 7333346: 7333346: 73333346: 7333346: 7333346: 7333346: 7333346: 7333346: 7333346: 73333346: 733336: 733336: 733336: 733336: 73336: 73336: 73336: 73336: 73336: 73336: 73336: 73336: 73336: 7336:

N

200

45:28

15:

16

Jul

Tue

```
length
                                                                                                                                                                                                                                                                                                                                                                                        ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                          leng
                                                                                                                                                                                                                                                                                                                                                               lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eng,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eng
                                                                                                                                                                                                                                                                                                                                                                                                                                            en
                  length
be in land length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in
gth
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ngth
P in
ingth
P in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp ir
lengt
bp j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lengt
38 bp i
1engt
17 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.
nown le.
10547 b
  of 3488
unknown
of 2455
unknown
of 3496
unknown
of 2758
unknown
of 3375
unknown
of 4119
unknown
of 3721
unknown
of 4212
unknown
of 3721
unknown
of 5182
unknown
of 5182
unknown
of 3891
unknown
of 3737
unknown
of 3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lown |
1888
lown |
0047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
of 5669
unknown
of 4899
unknown
of 6463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
of 6226
unknown
of 4590
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
of 7882
unknown
of 7398
unknown
of 7535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X T X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unkı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
un)
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: gap of unit gap
                                                                 gap of contig gap of
                               ig
of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 64
     ti
ti
                                                      ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                          gap
96442:
96542:
98997:
102593:
102593:
102693:
1086442:
108642:
108642:
108642:
112017:
1123902:
123902:
123902:
123902:
1240001:
12729:
123902:
123902:
123902:
1240001:
127293:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123902:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
123903:
92955
96443
96543
968443
98998
102594
102594
102594
102594
102594
102585
102585
102585
102585
1123003
1136034
1136034
1136034
1136034
1136034
1136034
1136034
1136034
1136034
1136034
1136034
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
127610
```

```
Н
                                                          9
                                                                         Ø
                                                                                        28
                                                                                                                                       \infty
                                                                                                                                                                     \boldsymbol{\sigma}
                                                                                                                                                                                                                                                  18406
                                                                                                                                                                                                                                                                                18394
                                                          1847
                                                                         1846
                                                                                                                                                                                                    18423
                                                                                                                                                                             1105
                                                                                                                                                                                                           1225
                                                                                                                                                             S
                                                                                                                                                                                                                           2
                                                  631
                                                                 691
                                                                                 751
                                                                                                       184
                                                                                                               865
                                                                                                                               925
                                           \mathbf{sd}
                                           Ga
                                                 agcagggagcctttggcctctccaagggaagcctagtgggcctagacccctcctcccatg
                                                                                                                              289579
                                           49
               23"
others
                                   Length
                                           Indels
               library
t 7399
                                  Score 643.2; DB 2
Pred. No. 1.4e-114
; Mismatches 163.
Ţ
                                          ó
                                  ch 36.9%;
il Similarity 81.3%;
920; Conservative
                    Ŕ
                                  Query Match
Best Local S
Matches 920
                   COUNT
                                                                 632
                                                         184805
                                                                                               752
                                                                                                                               866
                                                                        184745
                                                                                                               812
                                                                                                                                              926
                                                                                                                                                                            1046
                                                                                                                                                                                            1106
                                                                                        184685
                                                                                                       184627
                                                                                                                                      184526
                                                                                                                                                             986
                                                                                                                                                                                                           1166
                                                                                                                                                                                                                           1226
                                                                                                                                                     184467
                                                                                                                                                                                                                                          1286
                                                                                                                                                                                                                                                         1346
                                                                                                                                                                     84408
                                                                                                                                                                                    184348
                                                                                                                                                                                                                   184232
                                                                                                                                                                                                                                  184172
                                                                                                                                                                                                                                                                 184060
                                                                                                                                                                                                    84291
                                                                                                                                                                                                                                                  84120
                                                  57
                   BASE CO
                                                                                                                       184
                                                         ದ್ದ
                                                                                        g
                                                                                                       g
                                                                                                                       g
                                                                                                                                      ga
                                                  ò
                                                                                                                                                     Dρ
                                                                                                                                                                     Q
                                                                 õ
                                                                                ò
                                                                                               à
                                                                                                                                              ò
                                                                                                                                                                                    qq
                                                                                                                                                                                                                   a
                                                                                                               ô
                                                                                                                              ŏ
                                                                                                                                                             ŏ
                                                                                                                                                                             δ
                                                                                                                                                                                                                                  qq
                                                                                                                                                                                            δ
                                                                                                                                                                                                           δy
                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                         ò
```

a

ŏ

a

ò

```
op in
length
bp in l
                                                     bp in
length
                                                                        length
bp in le
length
bp in le
length
length
                                                                                                                                                                                                                                                                                                                                                                                                                             length
bp in l
length
bp in l
length
                                                                                                                                                                                                                                                                                             length
bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
bp in l
                                                                                                                                                                                                                                                                                                                                                 length
bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                     length
bp in l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
bp in l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in l
length
bp in l
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in l
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in l
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
bp in l
                                                                                                                                                                                                                                                   bp in
length
bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in
length
bp in
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lèngth
bo in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
bp in
                                                                                                                                                                                                                                                                                                                        lengt
bp ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp ir
lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leng
                                                                                                                                                          len
bp
len
bp
len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                len
bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dq
                                                                                                                                                    unknown of 2790 unknown of 2808 unknown of 2999 unknown of 2749 unknown of 2233 unknown of 3746 unknown of 3066 unknown of 3544 unknown of 3135 unknown
                                                                     unknown
of 2728
unknown
of 2060
unknown
of 2506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
of 4181
unknown
of 5568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
of 4454
unknown
of 4540
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 4005
unknown
of 5490
unknown
of 3364
unknown
of 5793
unknown
of 4240
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
of 4028
                  gap of contig gap of gap of contig gap of contig gap of contig gap of contig gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap or
contig
                                                                                                                            gap of contig gap of gap of contig gap of contig gap of contig gap of contig gap of gap of
                                                                                                                                                                                                                                        gap of contig gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of contig gap of contig gap of gap of gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of contig gap of contig gap of gap of gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of contig gap of contig gap of gap of gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
       contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of contig
  26620: 30876: 330876: 33188: 33288: 33188: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33288: 33228: 33228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 332228: 33228: 332228: 332228: 332228: 332228: 332228: 332228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 33228: 
   24603
26721
30777
30877
33189
33189
33189
33189
33189
33189
36117
36117
36117
36117
36117
36117
36117
36117
36117
36117
36117
49680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629680
629
                                                                                                                                                                                                                                                                 3 24-DEC-2001
DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry,
om 208, Norman
                                                                                                                                         183769
                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
Murinae; Mus
                              18388
                                                                                   18382
                                                          1585
                                                                                                              1645
   igaccgt
|||||||
                                                     NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                 HTG
                                                                                                                                                               AC104327
Mus musculus clone rp23-295a4 strain C57BL/6J, WORKING SEQUENCE, 66 unordered pieces.
AC104327
AC104327.2 GI:17978117
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Eutharia; Rodentia; Sciurognathi; Muridae; Mula, A. and Roe, B.A.

Hua, A. and Roe, B.A.

Mus musculus BAC Clone rp23-295a4

Unpublished

2 (bases 1 to 326750)

Hua, A. and Roe, B.A.

Direct Submission

Submitted (10-DEC-2001) Department of Chemistry And Bic The University of Oklahoma, 620 Parrington Oval, Room; OK 73019, USA

On Dec 24, 2001 this sequence version replaced gi:17439
gi:17
                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
bp in length
length
bp in length
length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24, 2001 this sequence version replaced g
------ Genome Center
: Department Of Chemistry And Biochemistry
iversity Of Oklahoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length bp in length length bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown of 2175 unknown of 2792 unknown of 2097 unknown of 2063 unknown of 3562 unknown of 2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of contig gap of contig gap of gap gap gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2180:
4455:
4555:
7347:
7447:
10157:
12254:
14517:
18179:
20239:
22342:
24502:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Department
The University Of (
Center code: UOKNOR
                                                                                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2181
2281
4456
4456
4556
7348
10058
10158
12255
14418
14418
18180
20240
20240
22343
22443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ******
                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                          183944
                                                                                                                                     183826
                                                                                                                                                                                                                                             AC104327
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

length

ţЪ

th

eng

engt.

ength p in

th

ength p in

th

eng

th

eng

length

th

length

in

length

tЪ

length

length

length

length

length

ength

ir Jth in length

length

th

length

length

eng

ťЪ

length

length

length

ength

Φ

Tu

2

 α

·rg

 \dashv

```
GI:14196230
                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                  MRNA
                                                                                                                                                                                                                                                                                                                                                                                          AB051678
Danio rerio m
AB051678
AB051678.1 (
                 5640
     866
                              926
                                          5699
                                                                                 1046
                                                                                                          1106
                                                                                                                                                195934
                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                        986
                                                                                                                                   1166
                                                                    195758
                                                                                              195818
                                                                                                                       195875
                                                                                                                                                             1226
                                                                                                                                                                                       1286
                                                                                                                                                                                                                 1346
                                                                                                                                                                                                                                         1406
                                                                                                                                                                                                                                                                   1466
                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                         195994
                                                                                                                                                                                                   196046
                                                                                                                                                                                                                                                                                            1526
                                                                                                                                                                                                                             196106
                                                                                                                                                                                                                                                      196166
                                                                                                                                                                                                                                                                                                                     1586
                                                                                                                                                                                                                                                                                                                                               1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                        196282
                                                                                                                                                                                                                                                                               196222
                                                                                                                                                                                                                                                                                                                                  96340
                                                                                                                                                                                                                                                                                                                                                          196398
                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
AB051678
LOCUS
                 19
                                           19
                g
                                                                                              q
                              ò
                                                                                 ò
                                                                                                                       a
                                                                                                                                                qq
                                                        õ
                                                                                                           ô
                                                                                                                                                                          qq
                                                                                                                                                                                                                             Ωp
                                                                                                                                    ò
                                                                                                                                                                                       ò
                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                               qq
                                                                                                                                                             ô
                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                            19557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19563
                                                                                                                                                                                                                                                                                                                                                                                                                   19553
                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                         1954
                                                                                                                                                                                                                                                                                                                                                                             691
                                                                                                                                                                                                                                                                                                                                                    631
                                                                                                                                                                                                                                                                                                                                                                                                      751
                                                                                                                                                                                                                                                                                                                                                                                                                                811
                                                                                                                                                                                                                                                                                                                                                                                                                                                         865
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                    gacc
                                                                                                                                                                                                                                                                                                                                                                GACC
                                                                                                                                                                                                                                                                                                                                                                            gttc
                                                                                                                                                                                                                                                                                                                                                                                    GCTC
                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                agccccaaacgggaacacctgccctggccgtgggcatcgccttcttcctcatgac
                                                                                                                                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                          326
                                                                                                    g or 7682 bp in length f unknown length g of 4151 bp in length g of 8033 bp in length g of 8033 bp in length g of 7605 bp in length g of 10360 bp in length f unknown length g of 8593 bp in length f unknown length g of 10742 bp in length f unknown length g of 7863 bp in length f unknown length g of 7863 bp in length f unknown length g of 7863 bp in length f unknown length
                                                                                                                                                                                                                                                                                          23"
others
                                                                                                                                                                                                                                              length.
                                                                                                                                                                                                                                                                                                                          Length
                                                                                     length
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                          cnown ic
21493 bp in
rn length
                                                                                                                                                                                                                                                                                          library
t 6725
              length
bp in 1
length
bp in 1
length
bp in 1
length
bp in 1
length
                                                                       bp in length bp in length length bp in length
                                                                                                                                                                                                                                       length
2 bp in
                                                                                                                                                                                                                                                                                                                       Score 642.2; DB 2;
Pred. No. 2.3e-114;
; Mismatches 164;
                                                                                                                                                                                                                         unknown leng
of 17968 bp
                                                                                                                                                                                                                                       unknown l
of 13352
       of 4414
unknown
of 5171
unknown
of 3840
unknown
of 9101
unknown
of 4567
unknown
of 5301
unknown
                                                                                                                                                                                                                                                                                                 ب
                                                                                                                                                                                                                                                                                          BAC 219 t
                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                          1. .326/50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="rp23-295a4"
/clone_lib="RPCI mouse B!
a 80488 c 78974 g 8121
                                                                                                                                                                                                                    of
                                    gap or
contig
                                                    gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig
       contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                    ;;
0
159547:
163961:
164061:
169232:
173172:
173272:
178880:
1782848:
198281:
1982848:
198281:
206031:
210282:
210382:
210382:
210382:
226120:
236580:
236580:
245373:
256115:
256115:
256115:
256115:
256115:
256115:
256115:
256115:
273737:
313398:
                                                                                                                                                                                                                                                                                                                        ch 36.8%;
l Similarity 81.2%;
919; Conservative
159448
159548
163962
164062
169333
173173
173273
173273
179081
198282
192849
192849
192849
198282
206032
206032
206032
210283
210383
218516
226221
226221
236581
245274
245274
245274
245374
256116
256216
256216
256216
33681
273638
                                                                                                                                                                                                                                                                                                Ø
                                                                                                                                                                                                                                                                                              9344
 ************
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 919
                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                               COUNT
                                                                                                                                                                                                                                                                                                                                                 572
                                                                                                                                                                                                                                                                                                                                                                                                  692
                                                                                                                                                                                                                                                                                                                                                                          632
                                                                                                                                                                                                                                                                                                                                                                                                                                         5539
                                                                                                                                                                                                                                                                                                                                                             195361
                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                195481
                                                                                                                                                                                                                                                                                                                                                                                                                            752
                                                                                                                                                                                                                                                                                                                                                                                                                                                     812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                   EATURES
                                                                                                                                                                                                                                                                                              BASE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Φ
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                         ga
                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
```

```
20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              display
                                                                                                                                                                                                S
                                                                                                                                                                                                                                                                                        196221
                                              S
                                                                                                         19587
                                              1957
                                                                                                                                                                                                19604
                56
                                                            ហ
                                                                                                                       1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi
Ostariophys
                                                                                                                                                                                                               1345
                                                                                                                                                                                                                                                                                                      1525
                               S
  92
                               981
                9
                                                                                                                                                                                                                                                                                                                                                                164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jourio rerio cDNA to mRNA.

Danio rerio
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostario
Cypriniformes; Cyprinidae; Danio.

(bases 1 to 1838)
Hirate,Y., Mieda,M., Harada,T., Yamasu,K. and Okamoto,H.
Identification of ephrin-A3 and novel genes specific to the midbrain-MHB in embryonic zebrafish by ordered differential
cctcttttgtcttctgtgaagacaggacctatgcaacgcacagacacttttggagaccgt
                                                                                                                                                                                                                                                                                                                                 19644
                                                                                                                                                                                                                                                                                                                                                                                                                                                VRT
                                                                                                                                                                                                                                                                                                                                                                                            169
                                                                                                                                                                                                                                                                                                                                                                                          linear
cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
complete
                                                                                                                                                                                                                                                                                                                                                                                                                                               1838 bp
ephrin-A3,
```

ρ

Ĭ.

ᅼ

56

33-7

09-7

ns

Φ

Tu

```
L Mechanisms of devc...

E 21412237
E 2 (bases 1 to 1838)
(S Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamocc,...
(S Hirate, Y., Mieda, M., Harada, T., Yamasu, K. and Okamocc,...

Birect Submission
AL Submitted (24-NOV-2000) Yoshikazu Hirate, Brain Science Institute,
RIKEN, Lab. of Developmental Gene Regulation; 2-1, Hirosawa,
Wako-shi, Saitama 351-0198, Japan (E-mail:hirate@brain.riken.go.jp,
Tel:81-48-467-9713, Fax:81-48-467-9714)

Location/Qualifiers

1838
----in rerio"
                                                                                                                                                                                          /product="ephrin-A3"
/product="ephrin-A3"
/protein_id="BAB55891.1"
/db_xref="GI:14196231"
/translation="MALYALCLFLLTLTCTNFALVTAARHAVHWNSSNILLRKEGYTL
OVNVNDYLDIYCPHYNSSQRGIAEQYVLYMVSYRGYRTCDPQLGFKRWECNRPHAPHA
PIKFSEKFQRYSAFSLGYEFHVGQEYYYISTPTHHHGRSCLRLRVYVCCSTASDSDDE
PQPTEPDYTLRPNIKIDDLDDYDNPEVPKLEKSISGSSPSRDRLLLTVASLLLIALSV
S"
                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1127
                                                                                                                                                                                                                                                                                                                                                                  138
                                                                                                                                                                                                                                                                                                                                                                                      680
                                                                                                                                                                                                                                                                                                                                                                                                         158
                                                                                                                                                                                                                                                                                                                                                                                                                             732
                                                                                                                                                                                                                                                                                                                                                                                                                                                 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 catggt
                                                                                                                                                                                                                                                                                                                                                                 caccgt
                                                                                                                                                                                                                                                                                                                                                                                                     CAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cagege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcactccgggggagaagccggtccccactctccccagttcaccatgggccccaatgtgaa
                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                        Length 1838
                                                                                                                                                                                                                                                                                                                                                             ccggccgcacgcacagccccatcaagttctcggagaagttccagcgctac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gatcaacgtgctggaagactttgagggagagaaccctcaggtgcccaagcttgag
                                                                                                                                                                                                                                                                                                                                                                                                                                             999ccccgggggcggggcccggaggcggggcagagcagtacgtgctgta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1174
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   catcagoggaccagocccaaacgggaacacctgcccctggccgtgg
                                                                                                                                                                                                                                                                                                                       Score 253; DB 5;
Pred. No. 4.5e-39;
; Mismatches 155;
                                                                                                                                                                                                                                                                                 469
                                                                                                                                                550. .1209
/gene="ephrin-A3"
550. .1209
/gene="ephrin-A3"
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                      14.5%;
nilarity 68.0%;
Conservative
                                                                                                                                                                                                                                                                                 O
                                                                                                                                                                                                                                                                                                                                1 Similarity 399; Conser
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
        JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                               COUNT
                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                 621
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                     139
                                                                                                                                                                                                                                                                                                                                                                                                                          681
                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1128
                                                                                                                                                                 CDS
                                                                                                     FEATURES
                                                                                                                                                                                                                                                                              BASE CO
                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ο
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <del>a</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ο
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
ROD 25-AUG-2001
                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="ephrin A3"
/protein_id="AAK92219.1"
/db_xref="GI:15290523"
/translation="CPHYNSSGPGGAEQYVLYMVNLSGYRTCNASQGSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGQEYYYISTPTHNLHWKCLRMKVFVCCASKDFEGENPQVPKLEKSISG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                   Vertebrata; Euteleostomi;
                                                                                                                           Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A., Jimenez,E., Varas,A. and Zapata,A.G.
Expression and function of the Eph A receptors and their ligands ephrins A in the rat thymus

L Unpublished

2 (bases 1 to 355)

Munoz,J.J., Alonso-C,L.M., Sacedon,R., Crompton,T., Vicente,A., Jimenez,E., Varas,A. and Zapata,A.G.

Direct Submission

L Submitted (13-JUL-2001) Cell Biology, Complutense University of Madrid, Av. Complutense, Madrid 28040, Spain

Location/Qualifiers
                                                                                                                                                                                                                                          of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                                  ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                    tyrosine kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  35
                                                                                                Chordata; Craniata; Vertebrata; E
Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                    cds
                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
,7;
37;
                                  partial
                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 241.8; DB ]
Pred. No. 5.7e-37;
; Mismatches 37
                                                                                                                                                                                                                                                                     1. .355
/organism="Rattus norvegicus"/db_xref="taxon:10116"
<1. .>355
/note="Eph-related receptor 1
                        355 bp
A3 mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                       64
                                  ephrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                       GI:15290522
                                                                                                                                                                                                                                                                                                                                                                                                                                              13.9%;
illarity 87.7%;
Conservative (
                                                                                   Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                Rattus norvegicus
AY045577
AY045577.1 GI:152
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                      AY045577
                                                                                                                     Rattus.
1 (base
                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
RESULT 13
AY045577
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C
                                                                                      ORGANISM
                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                  JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                      COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Loc
Matches
                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                         our
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320
                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                     BASE CC
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
```

RESULT

Tue

```
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search
Job time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                          ò
                                                                  q
                                                                                                                  qa
                                                                                                                                                                   qq
                                          δ
                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                        1. .2535
/organism="Mus musculus"
/strain="129"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/chromosome="3"
1. .2535
/gene="Epl3"
join(<926. .1215,1543. .1608,1793. .1870,2111. .2241)
/gene="Epl3"
/note="GPI-anchored ligand"
/codon_start=2
/product="LERK-3"
/protein_id="AAC39961.1"
/db_xref="GI:2843099"
/translation="LRREGYTVQVNVNDYLDIYCPHYNSSGPGGAEQYVLYMVNLSG
YRTCNASGSKRWECNRQHASHSPIKFSEKFQRYSAFSLGYEFHAGGEYYYISTPTHN
LHWKCLRMKVFVCCASTSHSGEKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKS
ISGTSPKREHLPLAVGIAFFLMTLLAS"
926. .1215
                -FEB-199
                                                                                                                                                      (Epl3),
2 (EPLG6):
                                                                                                      Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atat 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 25
                07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccagcacctgcggcgagaggctacaccgtgcaggtgaacgtgaacgactatctggatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acgc
                                                                                                                                                                 n-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --cAGGGCCTGGCGG
                                                                                 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri

1 (bases 1 to 2535)

Cerretti, D.P. and Nelson, N.

Characterization of the genes for mouse LERK-3/Ephrin-A3

mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A5

conservation of intron/exon structure

Genomics 47 (1), 131-135 (1998)

2 (bases 1 to 2535)

Cerretti, D.P. and Nelson, N.

Direct Submission

Submitted (11-MAR-1997) Molecular Biology, Immunex Corp.

University Street, Seattle, WA 98101, USA

Location/Qualifiers
                                                                                                                                                       -A3
                ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                        Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1870,2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2535
               linear
cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1608,1793
               DNA
partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 222; DB 10;
Pred. No. 4.8e-33;
; Mismatches 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545
           2535 bp
Mus musculus LERK-3 (Epl3) gene,
U92885.1 GI:2843000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(<926. .1215,1543
/gene="Epl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="LERK-3"
1543. .1608
/gene="Ep13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    926. .1215
/gene="Epl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=3
1793. .1870
/gene="Epl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2111. .2535
/gene="Epl3"
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%;
illarity 84.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=
                                                                             mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
271; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532
                                                                        house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 271
                         DEFINITION
                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                             ourc
                                                                                                                                                                                        JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                    ACCESSION
VERSION
                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980
                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                               FEATURES
U92885
LOCUS
                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
```

```
-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                               1135
                                                                                    1195
                                                                                                                                                                                                                                                                                           signa
                                                                                                                                                                                                                                                                                                                                                                                                                                               1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1684
        107
                           348
                                                                 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleos
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
60
                                                                                                                                                                                                                                                                                                                                                                                                                                               Endress, G.
                                                                                                                                                                                                                                                                                          screening using
                                                                                                                                                                          PAT
                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                         186
                                                                                                                                                                                                                           Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae

1 (sites)

Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Encentingan, S., Soppet, D.R. and Weaver, Z.

Cancer gene determination and therapeutic screening gene sets

Patent: Wo 0194629-A 2646 13-DEC-2001;

Avalon Pharmaceuticals (US)

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      others
                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Score 183.4; DB 6;
Pred. No. 1.2e-25;
; Mismatches 2;
                                                                                                                                                                           DNA
                                                                                                                                                                     Sequence 2646 from Patent W00194629. AX332137.1 GI:18122771
                                                                                                                                                                                                                                                                                                                                                                     u
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
. 34 c 61 g 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09:55:24
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                       10.5%;
al Similarity 98.9%;
184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch completed: July 13,
time: 4399 sec
                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggagat 1690
                                                                                                                                                                                                                                                                                                                                                                     49
                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGNT
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                             AX332137/c
LOCUS
                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                       15
                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                    1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
        1016
                                                                 349
                                                                                                                          1196
                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                            289
                                             1076
                                                                                                      409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                              JOURNAL
```

Appli Appli

Sequence | Sequence |

ALIGNMENT

```
RESULT 1
US-08-299-567-8
Sydenere 8, Application US/08299567
Patent No. 5747033
FEBRET INFORMATION:
FAPLICANT: Davis, et al.
TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL NUMBER OF SEQUENCES:
CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STARE: 177 Old Saw Mill River Road
CITY: Tartycown
STARE: New York
COUNTRY: US.A.
COMPUTER: New York
COUNTRY: US.A.
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
ATTORNEY/AGDNT INFORMATION:
RESERVATION NUMBER: 32, 143
RESTSTATION NUMBER: 32, 143
RESTSTATION NUMBER: 32, 143
REPERENCE/DOCKET NUMBER: REG 290
TELECOMMUNICATION INFORMATION:
RESERVATION FOR SEO ID NO: 8:
ELECHONE: 914-345-7400
SEQUENCE CHARACTERISTICS:
LENGTH: 1070 base pairs
    US-08-452-779-11

US-08-445-065-11

US-08-959-524-11

US-08-321-162-1

US-08-441-216-1

PCT-US95-15781-4

US-09-048-129-1

US-09-048-129-1

US-09-048-129-1

US-09-048-129-1

US-09-048-129-1

US-08-440-815-3

US-08-440-815-3

US-08-440-815-3

US-08-240-124-3

US-08-240-124-3

US-08-240-124-3

US-08-253-943-3

US-09-358-734-3

US-09-358-734-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 949.2;
Pred. No. 9e-1
0; Mismatches
         41421141144335114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 54.5%;
Local Similarity 97.0%;
les 976; Conservative
     1480
1480
1498
1498
1728
1728
1728
1839
1839
636
636
636
636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (ge
  Query Match
  228
330
331
332
334
336
336
447
443
                                                                                                                                       updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
                                                                                                                                                                                                    aaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.99 Seconds alignments)
Million cell u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l by chance to have
the result being pre
e distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Descript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequenc
                                                                                                                                                                                              .aaaaaaaaaaaaaaa
                                                                                                                                                                                                                                                                                                         767066
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ltd
                                                                                               arch time
(without
7929.972
    4.5
Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s predicted
e score of t
total score
                                                                                                Search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-453-943-1
US-09-057-121-1
US-09-358-734-1
US-09-358-734-1
US-09-324A-9
US-09-173-492-9
US-09-173-133-9
US-08-455-001-3
PCT-US95-11869-3
US-08-455-001-1
PCT-US95-11869-1
US-08-455-001-1
PCT-US95-11869-1
US-08-173-133-7
US-09-609-324A-7
US-09-173-492-7
US-09-173-492-7
US-09-173-492-1
US-09-173-133-1
                                                                                                                                                                                                                                                                                                   chosen parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299-567-8
                                                                                                                                                                                                                                                                         residues
   version
- 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                mode1
                                                                                              ••
                                                                                                                                                                                                                                                                                                                                                                                                               summaries
                                                                                              : 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
                                                                                                                                                                                    gctgctgctgctgctgc.
                                                                                                                                                                                                                                        1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l to the of the t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         results
                                                                                                                                                                                                                                                                   122816752
                                                                 Ŋ
                                                                                              : 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -80-
GenCore
(c) 1993
                                                                                                                                                                                                                                      Gapext
                                                              using
                                                                                                                                                                                                                                                                                                                                                                                             100%
45 St
                                                                                            08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sn
                                                                                                                                                                                                                                                                                                                              0
2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1037 1 05

1037 2 05

1037 2 05

1037 4 05

642 1 05

642 4 05

642 4 05

642 4 05

783 1 05

783 1 05

1809 5 PC7

1809 1 05

1809 5 PC7

314 4 05

314 4 05

555 4 05

555 4 05

555 5 PC7

1809 5 PC7

1809 1 05

1809 5 PC7

1809 5 PC7

1809 6 PC7

1809 7 05

1809 7 05

1809 7 05

1809 7 05

1809 7 05

1809 7 05

1809 8 PC7

1809 8 PC7

1809 8 PC7

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1809 1 05

1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analysis o
                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                           2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οŧ
                                                                                                                                                                                                                                                                                               satisfying
                                                                                                                                                                                                                                                                                                                                                                            Match
Match
first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 ,
                                                                                                                                                                                                                                                                    seds,
                                                                                                                                                     US-09-733-75
1743
1 gctqctqcta
                                                            search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number
              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1070
                                                                                         13,
                                                                                                                                                                                                                                                                                                                                                                         Minimum
Maximum
Listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    than
                                                                                                                                                                                                                                                               383533
                                                                                                                                                                                                                                                                                                                                                                                                                                            ssued
                                                                                                                                                                                                                                                                                                                            length:
length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρλ
                                                                                      July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 949.2 54.5

917.8 52.7

917.8 52.7

917.8 52.7

149.2 8.6

149.2 8.6

149.2 8.6

149.2 8.6

149.2 8.6

149.2 8.6

139.6 8.0

139.6 8.0

135.4 7.8

135.4 7.8

135.4 7.8

135.4 7.8

128.8 7.4

128.8 7.4

128.8 7.4

128.8 7.4

128.8 7.4
                                                           nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                              hits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. is the greater t]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                        H 20 M 4 50 9
                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                     Post-processing
                                                                                                                                                                                                                                                                                                                             sed
                                                                                                                                                                   score
                                                                                                                                                                                                                table
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core
                                                                                                                                                                                                                                                                                             number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             score gand is
                                                      nucleic
                                                                                                                                                                                                                                                                                                                          DB
DB
                                                                                                                                                Title:
Perfect sc
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                            Searched
                                                                                                                                                                                                                                                                                                                       Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                       Φ
                                                                                   Run on:
                                                                                                                                                                                                             Scoring
                                                                                                                                                                                                                                                                                                                                                                                                                                    Databas
                                                                                                                                                                                                                                                                                           Total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255
25
25
26
27
27
27
27
27
27
27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                       ŏ
```

Ϊ;

Gaps

12;

Indels

1070

DB 1; -186;

; 0

Best Loc Matches

-

οy

Sequence Sequence Sequence Sequence Sequence

ednence

09

a

9

Version

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OP/CLATION NUMBER

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System: Apple System:

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE

WASHINGTON: USA

98101

COUNTRY:

STATE: WASTE

APPLICATION NUMBER: US 08/161,132 FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA:

FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/114 FILING DATE: 30-AUG-1993 PRIOR APPLICATION DATA:

3 •• Ю 4 ** S Η

9 -

h

ò

ŏ

ò

d

g

ò

ò

g

g

g

Q

à

g

ò

g

ö

a C

q

õ

q

ò

òγ

g

ò

```
120
             180
                          240
                    239
                                 287
                                       300
                                                    360
                                                                                                                                                                                        1007
                                             347
                                                                 420
                                                          407
                                                                      467
                                                                             480
                                                                                  527
                                                                                          540
                                                                                                      900
                                                                                                            647
                                                                                                                  099
                                                                                                                               :720
                                                                                                587
                                                                                                                         707
                                                                                                                                            780
                                                                                                                                                        840
                                                                                                                                     767
                                                                                                                                                                     900
                                                                                                                                                                                 096
                                                                                                                                                  827
                                                                                                                                                              887
 tgcg
              cgca
        TGCG
                 CGCA
                              ||||||
AGCA
                                     agca
                                                               gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                             cgt
                                                                                   CGT
                                                                                                     ggc
|||
                                                                                          cac
                                                                                             CAC
                                                                                                                         CGC
                                                                                                                              tct
                                                                                                                                                              TCT
                                                                                                                                                                     999
                                                                                                                                                                           GNG
                                                                                                                                                                                agcctagtgggcctagacccctcctccatggctagaagtggggcctgcaccataca/
20
61
            121
                  80
                         181
                               240
                                      241
                                            288
                                                        348
                                                  301
                                                                     408
                                                                           421
                                                                                  468
                                                                                              528
                                                                                                                                    708
                                                               361
                                                                                        481
                                                                                                     541
                                                                                                           588
                                                                                                                 601
                                                                                                                        648
                                                                                                                              661
                                                                                                                                          721
                                                                                                                                                768
                                                                                                                                                       781
                                                                                                                                                             828
                                                                                                                                                                   841
                                                                                                                                                                                      948
                                                                                                                                                                                            961
                                                                                                                                                                         888
                                                                                                                                                                                                  0.08
                                                                                                                                                                                901
      g
                  q
                               ga
```

APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELEPHONE: (206) 587-0430
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs

CDNA to mRNA

TOPOLOGY: linea MOLECULE TYPE: CDI HYPOTHETICAL: NO

single

STRANDEDNESS

nucleic acid

TYPE

sig_peptide 83..139

NAME/KEY: LOCATION:

FEATURE:

..799

NAME/KEY: LOCATION:

FEATURE

FEATURE:

hek-L A2

SOURCE:

ANTI-SENSE: IMMEDIATE SC

```
276
                                                        9
                                                       ó
                                1037
                                Length
                                            Indels
                               Score 917.8; DB 1;
Pred. No. 2.4e-179;
); Mismatches 2;
                                           ;
0
                               52.7%;
llarity 99.8%;
Conservative
mat_peptide
140..796
                              Query Match
Best Local Similarity
Matches 919; Conser
NAME/KEY:
LOCATION:
S-08-240-124-1
                                                                   97
                                                        -4
                                                                                61
                                                                                                         121
                                                                                            57
                                                                                                                     217
                                                                   qq
                                                                                δ
                                                                                            d
                                                                                                         ô
```

SURFACE

CELL

THE

BINDS

P. THAT

RESULT 2
US-08-240-124-1
; Sequence 1, Application US/08240124
; Patent No. 5516658
; GENERAL INFORMATION:
 APPLICANT: BECKMANN, M. P.
 APPLICANT: CERRETTI, DOUGLAS P.
 TITLE OF INVENTION: CYTOKINE TE

ö

.rni

33

60-

us

 $\mathbf{\Phi}$ Tu

```
240
                      300
            336
                                396
                                          360
                                                   456
                                                                                480
                                                                                                   540
                                                                                                            636
                                                                                                                       600
                                                                                                                                969
                                                                                                                                          99
                                                                                                                                                   756
                                                                                                                                                             720
                                                                                                                                                                       816
                                                                                                                                                                                 780
                                                                                                                                                                                                    840
                                                                                                                                                                                                                       900
   1999ctt
||||||||||
|GGGCTT
                                                            ggagaa
                                                                                                                      tcaggt
||||||
TCAGGT
                                                                                                                                          cctggc
||||||
                                                                                                                                                             secetg
||||||
                                                   GGAGAA
                                                                             caagcgctgggagtgcaaccggccgcaccgcacagccccatcaagttctcc
SURFACE
                                                                                                                                                                                                                                                                                                     CELL
                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                    BINDS
                                                                                                                                                                                                                                                                                      APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT BI
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                           US/0845394
                                                                                                                                                                                                                                         921
                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         Sequence 1, Application
Patent No. 5738844
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      -453-943-1
                             337
181
         277
                    241
                                                397
                                       301
                                                          361
                                                                    457
                                                                             421
                                                                                       517
                                                                                                 481
                                                                                                          577
                                                                                                                                                                                                                                                  697
                                                                                                                    541
                                                                                                                             637
                                                                                                                                                697
                                                                                                                                                          661
                                                                                                                                        601
                                                                                                                                                                    757
                                                                                                                                                                                       817
                                                                                                                                                                                                          877
                                                                                                                                                                              721
                                                                                                                                                                                                 781
                                                                                                                                                                                                                    841
                                                                                                                                                                                                                              937
                                                                                                                                                                                                                                        901
                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                     -08
         Op
                                                g
                   ò
                             Q
õ
                                       ò
                                                          õ
                                                                    a
                                                                                       q
                                                                                                                             qq
                                                                             δ
                                                                                                ò
                                                                                                          a
                                                                                                                                                g
                                                                                                                    ò
                                                                                                                                       ò
                                                                                                                                                                    d
                                                                                                                                                          ò
                                                                                                                                                                                       a
                                                                                                                                                                                                           g
                                                                                                                                                                              ð
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                              q
                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                        ò
```

```
216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 917.8; DB 1;
Pred. No. 2.4e-179;
); Mismatches 2;
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple System 7.1
SOFTWARE: Microsoft Word for Apple,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,943
FILING DATE: 30-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/240,124
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
"ETTER OF TELEFAX: (206) 233-0644
                   SYSTEM: Apple System 7.1
Microsoft Word for Apple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.8%;
Matches 919; Conservative
                                                                                                                                                                                                                                                                                                                                          1037 base pair
                                                                                                                                                                                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
83..139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
140..796
                                                                                                                                                                                                                                                                                                                                                                                           CDNA to
                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                      LENGTH: 1037 base
TYPE: nucleic aci
STRANDEDNESS: sir
TOPOLOGY: linear
MOLECULE TYPE: cDN
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L A2
                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
S-08-453-943-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

ö

disk

FORM:

Φ

Tu

g

ò

ò

Op

ò

q

q

ò

qq

ò

g

õ

ò

Op

d

ŏ

g

ŏ

qq

οy

Op

on the finite the fix the fix

ò

```
360
                    456
                                    420
                                                                                 576
                                                   516
                                                                   480
                                                                                                   540
                                                                                                                  636
                                                                                                                                  600
                                                                                                                                                 969
                                                                                                                                                                 9
                                                                                                                                                                               756
                                                                                                                                                                                                720
                                                                                                                                                                                                                                             876
                                                                                                                                                                                                                                                              840
                                                                                                                                                                                                               816
                                                                                                                                                                                                                               780
                                                                                                                                                                                                                                                                             936
                                                                                                                                                                                                                                                                                             900
                                                                                                                                                                                                                                                                                                            966
gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                   ttcgt
                                                                           TTCGT
                                                                                                                                 caggt
||||||
|CAGGT
                                                                                             ctggc
||||||
CTGGC
                                                                                                                                                                                                                                                                                         SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . la
                                                                                                                                                                                                                                                                                                                                                                                                                        CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version
                                                                                                                                                                                                                                                                                                                                                                                                                        THE
                                                                                                                                                                                                                                                                                                                                                                                                                        BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple £_stem 7.1
SOFTWARE: Microsoft Word for Apple, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,121
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION STA:
APPLICATION NUMBER: 08/240,124
                                                                                                                                                                                                                                                                                                                                                                   US-09-057-121-1

Sequence 1, Application US/09057121

Sequence 1, Application US/09057121

Patent No. 5969110

GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT ITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               P.
THAT
                                                                                                                                                                                                                                                                                                                                        1017
                                                                                                                                                                                                                                                                                                                          921
                                                                                                                                                                                                                                                                                                                         361
301
                397
                                               457
                                                                421
                                                                              517
                                                                                                                                                                                                                                                                                                                                       266
                                                                                               481
                                                                                                               577
                                                                                                                              541
                                                                                                                                             637
                                                                                                                                                                                            661
                                                                                                                                                                                                                                                                                         841
                                                                                                                                                             601
                                                                                                                                                                             697
                                                                                                                                                                                                           757
                                                                                                                                                                                                                                          817
                                                                                                                                                                                                                                                                                                                         901
                                                                                                                                                                                                                           721
                                                                                                                                                                                                                                                          781
                                                                                                                                                                                                                                                                          877
                                                                                                                                                                                                                                                                                                         937
                                                                                                                                                                                                                                                                                                                                                               RESULT
US-09-(
```

```
120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                               gttccagcgctacagcgccttctctctgggctacgagttccacgccggccacgagtacta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctacatctccacgcccactcacaacctgcactggaagtgtctgaggatgaaggtgttcgt
                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                            1037
                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                          Score 917.8; DB 2,
Pred. No. 2.4e-179,
); Mismatches 2,
FILING DATE:

APPLICATION NUMBER: US 08/161,132
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/114,426
FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.8%;
Matches 919; Conservative
                                                                                                                                                                                                                                                                                                                sig_peptide
83..139
                                                                                                                                                                                                                                                                                                                                             mat_peptide
140..796
                                                                                                                                                                                                                               CDNA to
                                                                                                                                                                                                                                                                                      CDS
83..799
                                                                                                                                                                                                                                                                   hek-L A2
                                                                                                                                                                                                                                       S
                                                                                                                                                                                               TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
                                                                                                                                                                                                                                                        SOUR
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
3-09-057-121-1
                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                              ANTI-SENSE: IMMEDIATE S
                                                                                                                                                                                                                                                                   CLONE:
                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

ö

```
540
           9
                                      989
                                                    600
                                                                  969
                                                                                099
                                                                                              756
                                                                                                             720
                                                                                                                                                                     840
                                                                                                                           816
                                                                                                                                          780
                                                                                                                                                       876
                                                                                                                                                                                                 960
                                                                                                                                                                                    93
                                                                                                                                                                                                                66
                                                                                sectage
||||||||
                                                                                                             cccctg
                                                                                                                                         aaggga
|||||||
SURFACE
                                                                                                                                                                                                                                                                                                                 BINDS THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                  Version
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Apple System 7.1

SOFTWARE: Microsoft Word for Apple, Ve

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/358,734

FILING DATE:

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/109,745
FILING DATE: 20-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SEESE, KATHRYN A.
                                                                                                                                                                                                                                                                                                BECKMANN, M. P.
CERRETTI, DOUGLAS P.
NVENTION: CYTOKINE THAT B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBER: US 08/114,426
30-AUG-1993
                                                                                                                                                                                                                                                                          Sequence 1, Application US/09358734

Patent No. 6274117

GENERAL INFORMATION:
APPLICANT: BECKMANN, M. P.
APPLICANT: CERRETTI, DOUGLAS P.
TITLE OF INVENTION: CYTOKINE THAT I
TITLE OF INVENTION: RECEPTOR HEK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/240,124
                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER
                                                                                                                                                                                                                                                             RESULT 5
US-09-358-734-1
       517
                     481
                                  577
                                                  541
                                                                637
                                                                                                                                                                                                                           901
                                                                                            697
                                                                                                                                      721
                                                                                                                                                                                877
                                                                                                                                                                                                                                        997
                                                                              601
                                                                                                          661
                                                                                                                        757
                                                                                                                                                    817
                                                                                                                                                                  781
                                                                                                                                                                                                             937
                                                                                                                                                                                               841
                                  a
                     ò
                                                 δ
                                                               qq
                                                                             δ
                                                                                            ದ್ದ
                                                                                                                        ga
                                                                                                                                      Q
                                                                                                                                                    qq
                                                                                                                                                                                g
                                                                                                                                                                                                             qq
                                                                                                          õ
                                                                                                                                                                  δ
                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                         qq
                                                                                                                                                                                               Š
```

```
Ga
                                                                                                                                                                                                                                                  ctgctgcgcctccacatcgcactccggggagaagccggtccccactctcccccagttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catgggccccaatgtgaagatcaacgtgctggaagactttgagggagagaccctcaggt
                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                       1037
                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                      Score 917.8; DB 4
Pred. No. 2.4e-179
; Mismatches 2
         ပု
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2814-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEKX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                    ó
                                                                                          mRNA
                                                                                                                                                                                                                      ch 52.7%;
I Similarity 99.8%;
919; Conservative
                                                                                TOPOLOGY: linear
MOLECULE TYPE: cDNA to m
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: hek-L A2
                                                                                                                                                                                 mat_peptide
140..796
                                                                                                                                                           sig_peptide
33..139
                                                                           single
                                                                                                                                           ...799
                                                                                                                                     CDS
83.
                                                                 TYPE: nuclei
STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                             ωœ
                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
9-358-734-1
                                                                                                                                                                                                                     Query Match
Best Local S
Matches 919
                                                                                                                     CLONE:
FEATURE:
                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                   7
                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                         277
                                                                                                                                                                                                                                                                                                                                                                                      337
                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637
                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541
                                                                                                                                                                                                -08
                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                 ō
                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

S

156

9

216

80

276

240

336

300

396

360

456

420

480

576

540

636

009

Tue

g

d

ò

ò

d

g

õ

ŏ

g

ò

g

306

340

366

400

457

```
208
                                                                                                                                                                                            RESULT
                                    qq
                                                                   g
                                                                                                    g
                                                                                                                                   ga
                                                     ò
                                                                                    ò
                                                                                                                     ò
                                                                                                                                                    ŏ
                                720
                   756
   099
                                                  816
                                                                   780
                                                                                                   840
                                                                                                                                  900
                                                                                   876
                                                                                                                   936
                                                                                                                                                   966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          642
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.2;
3. 4e-22;
5. 4e-22;
                                                                                                                                                                                                                                                          9-
                                                                                                                                                                                                                                                 P.
DESIGNATED LERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 149.2;
Pred. No. 4e
                                                                                                                                                                                                                                                                         ,324A
                                                                                                                                                                                                                    Sequence 9, Application US/09609324A; Patent No. RE37582; GENERAL INFORMATION:
APPLICANT: CERRETTI, Douglas P.
TITLE OF INVENTION: CYTOKINE DESIGNATED FILE REFERENCE: A7772; CURRENT APPLICATION NUMBER: US/09/609,32; CURRENT FILING DATE: 2000-06-30; PRIOR FILING DATE: 1997-08-29; PRIOR FILING DATE: 1995-10-03; PRIOR FILING DATE: 1995-10-03; PRIOR FILING DATE: 1994-10-05; NUMBER OF SEQ ID NOS: 10; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.8%;
Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(639)
NAME/KEY: mat_peptide
LOCATION: (88)..(639)
S-09-609-324A-9
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                : CDS
                                                                                                                                                                                                               -609-324A-9
                                                                                                                                                                                                                                                                                                                                                SOFIWARE.
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                         9
                 697
                                                                                                                                               937
                                                                                                781
                                                                                                               877
                                                                                                                                                               901
                                               757
                                                                721
                                                                                                                                                                               997
                                661
                                                                                 817
                                                                                                                                 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                        RESULT
US-09-6
```

```
ggaggcggggcagagcagtacgtgctgtacatggtgagccgcaacggctaccgcacctgc
                                    -ggggcgccgctgccgccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 642
                                                                                                                                                                                                                      #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440B
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 149.2; DI
Pred. No. 4e-22
                                                                                                                                                                                                                                                                                                                                                P.
Designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1997
                                                                                                                                                                                                                                                                                                                            ALTLE OF INVENTION: Cytokine Design NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation STREET: 51 University Street CITY: Seattle STATE: WA
COUNTRY: USA
                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08920440B
Sequence 9, Application US/08920440B
Patent No. 5919905
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2826-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.6%;
gacatctactgcccgcactat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 642 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11642
Signal
1-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION:
; NAME/KEY:
; LOCATION:
US-08-920-440B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                              307
                                                                                                                                                                                                                                            487
                      224
                                               247
                                                                     284
                                                                                                                                                                       401
                                                                                                                       341
                                                                                                                                              367
                                                                                                                                                                                              427
                                                                                                                                                                                                                      458
```

DB

Similarity

Local

147

121

62

ŏ

qa

88

qq

122

ò

148

Op

164

ò

163

tctg

207

cctg

223

gatatttactgcccgcactacaacagctcgggggtgggccccgggggcgggaccggggccc

-7 \sim 3 7 ı 9 0

1 S

```
98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 981
   INFORMATION
                                                                                                                                                              7
                                                                                                                                               Matches
                                                                                                                                                                             28
                                                                                                                                                                                            62
                                                                                                                                                                                                         88
                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                      164
                                                                                                                                                                                                                                                                    208
                                                                                                                                                                                                                                                                                   224
                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                                                                              341
                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                        458
                                                                                                                                                                                                                                                                                                                                                                                         427
                                                                                                                                                                                                                                                                                                                                                                                                                      487
                                                                                                                                                                             g
                                                                                                                                                                                           ò
                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                    αa
                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                  Óγ
                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                              ДQ
                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                        ò
   4;
                                                             14.7
                                                                            163
                                                                                                          223
                                                                                                                        246
                                                                                                                                       283
                                                                                                                                                      306
                                                                                                                                                                     340
                                                                                                                                                                                                  400
                                                                                          207
                                                                                                                                                                                   366
                                                                                                                                                                                                               426
   Gaps
                               87
                 61
                                           aggece
                               GACGCC
                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                          38
              S
                                                                                                                                                                                                                                                         Indels
 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09173492
Patent No. 6194172
GENERAL INFORMATION:
APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Designated LERK-6
NUMBER OF SEQUENCES: 10
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/920,440 FILING DATE: 29-AUG-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/173,492
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,347
3R: 2826-B
                                                                                                                                                                                                                                                                                                                                                               E: Immunex Corporation
51 University Street
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 28;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Cor
STREET: 51 University
CITY: Seattle
STATE: WA
COUNTRY: USA
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
329;
                                                                                                                                                                                                                                                                                             RESULT 8
US-09-173-492-9
                              28
                                            62
                                                                                        148
                                                                                                       164
                                                                                                                                                                  284
                                                                                                                                                                                                                                          427
                                                           88
                                                                          122
                                                                                                                      208
Matches
                                                                                                                                    224
                                                                                                                                                   247
                                                                                                                                                                                 307
                                                                                                                                                                                               341
                                                                                                                                                                                                              367
                                                                                                                                                                                                                            401
                             g
                                                          a
                                                                                        qq
                                             δ
                                                                          õ
                                                                                                        ã
                                                                                                                      a
                                                                                                                                                   g
                                                                                                                                                                                Db
                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                         ò
                                                                                                                                    Q
                                                                                                                                                                  ð
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                         q
```

```
246
                                                                                                                                                                                                                                                                                                                                           340
                                                                                                                                                                                                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                                                                                          426
                                                                                                                                                                                                                                                                                                                                                                                                          457
                                                                                                                                                              Gaps
                                                                                                                                                                             61
                                                                                                                                                                                            87
                                                                                                                                                                          -- GGGGGGCGCTGCCGCCG
                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                             \sim
                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                       158;
                                                                                                                                              4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.
Designated LERK-6
                                                                                                                                              DB
                                                                                                                                            Score 149.2; Dl
Pred. No. 4e-22
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cerretti, Douglas P.
TITLE OF INVENTION: Cytokine Desig
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/0917313. Patent No. 6232447
GENERAL INFORMATION:
                                                                                                                                                            ö
                                                     mRNA
                                                                                    CDS
11642
Signal Peptide
1-90
                                                                                                                                                                                                                                                                                           GACATCTACTGCCCGCACTAT --
    6
                                                                                                                                            8.6%;
ilarity 61.8%;
Conservative
                    642 base pairs
nucleic acid
SEQUENCE CHARACTERISTICS
LENGTH: 642 harm
                                     single
                                                     CDNA to
                                             linear
                                                                                                                                                    Local Similarity
es 329; Conser
                                                   MOLECULE TYPE: CI
                          TYPE: nuclei
STRANDEDNESS:
TOPOLOGY: li
                                                                                           LOCATION:
NAME/KEY:
LOCATION:
US-09-173-492-9
                                                                    ANTI-SENSE:
FEATURE:
                                                                                     NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-173-133-9
                                                                                                                                            Query Match
Best Local
```

.rni

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                   163
                                                                                                                                                                                                                                                                                                                                                                                                                                 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                       CTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                sctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGCCC
                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacgccggccacgagtactactacatt---ccacgcccactcacaacctgcactg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509
                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                       Length 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgtctgaggatgaaggtgttcgtctgctgcgcctccacatcgcactccgggg
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                       158;
                                                                                                                                                                                                                                                                                                                                     Score 149.2; DB 4;
Pred. No. 4e-22;
); Mismatches 158;
                                      Version
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/920,440
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                     US/09/173,133
       MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: System 7.6
SOFTWARE: Patentin Release #1.0,
                                                                                                                                         Ħ
                                                                                                                                        2826-
                                                                                                                  NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2826
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                  CDNA to mRNA
                                                                                                                                                                                                                                                                     CDS
11642
Signal Peptide
1-90
                                                                                                                                                                                                                                                                                                                                     8.6%;
Similarity 61.8%;
29; Conservative
                                           CURRENT APPLICATION DATA
APPLICATION NUMBER: US
FILING DATE:
FORM:
READABLE
TYPE: Fl
                                                                       CLASSIFICATION:
                                                                                                                                                                                                                               MOLECULE TYPE: CI
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
; NAME/KEY:
; LOCATION:
US-09-173-133-9
                                                                                                                                                                                                                                                                                                                                                     329;
                                                                                                                                                                                                                                                  ANTI-SENSE
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458
```

QO

ŏ

qq

α

g

ò

q

ŏ

g

q

Qγ

ŏ

qq

Q

ò

ŏ

```
gctgctcgtgcccgtgccgctgccgctgctggcccaagggcccggaggggcgctggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GCTGCTCGCCGCGATCGTCGGCGTCTGCGAGGGGACGACCCCGGCAAAGTGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aaaccggcatgcggtgtactggaacagctccaaccagcacctgcggcgagagggctacac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGACCGCTACGCCGTCTATTGGAACCGCAGCACCCCAGGTTCCACCGCGGGGGTTACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgtgcaggtgaacgtgaacgactatctggatatttactgcccgcactacaacagctcggg
                   538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 783;
                                                                                                                                                                        APPLICANT: Cheng, Hwai-Jong
TITLE OF INVENTION: EPH Receptor Ligands, and Uses Related
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
487 TGCCTGCGACTGAAGGTGTACGTGCGGCCGACCAACGAGACCCTGTACGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 149.2; DB 1;
Pred. No. 4.2e-22;
                                                                                                                                                                                                                                                                                                                                       COUNTER READABLE FORM:

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,001
FILING DATE: 31 MAY 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 base pairs
TYPE: nucleic acid
                                                                                                    Sequence 3, Application US/08455001
Patent No. 5795734
GENERAL INFORMATION:
APPLICANT: Flanagan, John G.
APPLICANT: Cheng, Hwai-Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sch 8.6%;
il Similarity 63.3%;
276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
86..148
                                                                                                                                                           Flanagan,
Cheng, Hwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3'UTR
686..783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
86..685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'UTR
1..85
                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
5-08-455-001-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                         -001-3
                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                     US-08-455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                     RESULT
```

279

255

312

9

```
GTCTCCCCCGAACGTG
                                                                                                                                                                                                                                                 gcccactcacaacctg
                                                                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (() INFORMATION FOR
                                                                                                                                                                                                                                                                                            RESULT 12
US-08-308-814-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                               169
                                                                                  229
                            92
                                                                136
                                                                                                    196
                                                                                                                                                        325
                                                                                                                                                                                           385
           109
                                                                                                                     280
                                                                                                                                       256
                                                                                                                                                                           313
                                                                                                                                                                                                                              445
                                                                                                                                                                                                                                                                  505
                                                                                                                                                                                                             373
                                                                                                                                                                                                                                                433
                                               g
                                                                                                                                                        g
                                                                                                                                                                                           a
                             ò
                                                                 Q
                                                                                  g
                                                                                                                     qq
                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                  Dp
                                                                                                    ò
                                                                                                                                       ò
                                                                                                                                                                                                             à
                                                                                                                                                                                                                                               ò
                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                    255
                                                                                          372
                                                                         384
                                                                                                                             432
                                                                                                                                               504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                 --GGAGCCGCTGCCCGCCGAGCGCATGGAGCGCTACGTCCTCTACAT
                                                                                                                         gcgcta
                                                                                                            GCTCTT
                                                                                        Length 783
                                                                                                                                                                                                                                                        and Uses Related
CGTGGAGGTGAGCATCAATGACTACCTGGACATCTACTGCCCTCACTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 149.2; DB 5;
Pred. No. 4.2e-22;
0; Mismatches 133;
                                                                                                                                                                                                                                                  EPH Receptor Ligands,
Thereto
5
                                                                                                                                                                                                                                                                                                                                                                       36,709
R: HMI-011CPPC
                                                                                                                                                                                                                                         APPLICANT:

TITLE OF INVENTION: EPH Receptor Ligar
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          Sequence 3, Application PC/TUS9511869 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         ATTURNEL/AGENT INFOLMATION.

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HMI-(
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 783 base pairs

TYPE: nucleic acid

STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.3%;
Matches 276; Conservative
                                                                                                                                                                         505 GTCTCCCCCGACGTG 520
                                                                                                                                                               gcccactcacaacctg 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
86..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'UTR
686..783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86..685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'UTR
1..85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                         RESULT 11
PCT-US95-11869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY:
; LOCATION:
PCT-US95-11869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATUR
229
                  196
                                                                      325
                                    280
                                                     256
                                                                                        313
                                                                                                         385
                                                                                                                                                              433
d
                 ò
                                  g
                                                                      qq
                                                                                                         a
                                                                                                                                            Q
                                                                                        ò
                                                                                                                                                                              q
                                                     ŏ
                                                                                                                           ò
                                                                                                                                                              ò
```

448

520

```
Related
                                                                                                                  Uses
                                                                                                                  and
                                                                                                                  Ligands,
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII(txt)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,814
FILING DATE: 19-SEP-1994
CLASSIFICATION: 435
Sequence 1, Application US/08308814
; Sequence 1, Application US/08308814
; Patent No. 6268476
; GENERAL INFORMATION:
    APPLICANT: Flanagan, John G.
    APPLICANT: Cheng, Hwai-Jong
    TITLE OF INVENTION: EPH Receptor Li
    TITLE OF INVENTION: Thereto
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD
    STREET: 60 State Street

                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: HM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 227-74 TELEFAX: (617) 227-5941 FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1615 base pairs
nucleic acid
DNESS: both
                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: bot
TOPOLOGY: linear
MOLECULE TYPE: CDNA
```

ctggg

getgetegtgeeegtgeegetgeegetgetgetegeeeaagggeeeggaggggee

```
0S-08
                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                              οy
                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                    3;
                                                                                                                                                                                                                                 339
                                                                                                                                                                                                     282
                                                                                                                                                                                                                   302
                                                                                                                                                                                                                                               362
                                                                                                               120
                                                                                                                                                           203
                                                                                                                                            162
                                                                      Gaps
                                                                                   9
                                                                                                                                                                                                                                                            cggaggggggctgggaaaccggcatgcggtgtactggaacagctccaaccagcacctgcg
                                                                                                                                                                                                    GGCCCGGGCCAACGCTGACCGATACGCAGTCTACTGGAACCGTAGCAACCCCAGGTTTCA
                                                                                                                                                                       24 GCGCCCGCTGCTGCTGCTGCTGCTGCTGCCGCTGCGTGCGCGCGCAACGAGGACCC
                                                                     42;
                                                       1615
                                                                                                                                                                                                                                                                                                                                                                              Related
                                                                                                                                                                                                                                                                                                       470
                                                       Length
                                                                      Indels
                                                                                                                                                                                                                                                                                        and Uses
                                                       Score 139.6; DB 4;
Pred. No. 4.7e-20;
; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                              Ligands,
                                                                                                                                                                                                                                                                                                                                           MBER: US/08/455,001
31 MAY 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII (text)
                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Vincent, Matthew P
                                                        8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARE: ASCII (text)
APPLICATION DATA:
                                                                      Conservative
                    sig_peptide
10..69
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 31 MA
       10..636
                                                              al Similarity
292; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            02109
                  ;
;
;
;
US-08-308-814-1
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-455-001-1
                                                        Query Match
Best Local
              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT
                                                                                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                        423
                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                     243
                                                                                                                  61
                                                                                                                                84
                                                                                                                                                                           163
                                                                                                                                                                                         204
                                                                                                                                                                                                                                   283
                                                                                                                                              121
                                                                                                                                                             144
                                                                       Matches
```

Ω

ò

Д

ò

a

ò

C

qq

ò

Пp

õ

```
EPH Receptor Ligands, and Uses Related
Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                           Score 139.6; DB 1;
Pred. No. 4.8e-20;
); Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
PCT-US95-11869-1
; Sequence 1, Application PC/TUS9511869
; GENERAL INFORMATION:
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                            8.0%;
illarity 62.4%;
Conservative
                                                                                                                                                                                                 sig_peptide
255..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORM:
                                                                                                                                                                        3'UTR
892..1809
                                                                                                                    CDS
265..891
                                                                                both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FOR
                                                                                                   CDNA
                                                                                                                                                      ..264
                                                                                          linear
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 292; Conser
                                                                                                                                             5'UTR
1..26
                                                                                STRANDEDNESS TOPOLOGY: 1
                                                                                                  MOLECULE TYPE:
                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                 NAME/KEY:
LOCATION:
3-455-001-1
                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                       FEATURE:
                                                                                                                                                                FEATURE:
                                                                                                                                                                                           FEATURE:
                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
                                                                                                                                                                                                                                                                                                                                                                                                                                           498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   678
                                                                                                                                                                                                                                                                                                                                                                     399
                                                                                                                                                                                                                                                                                                                                                                                        163
                                                                                                                                                                                                                                                                                                                                                                                                         459
                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
```

339

617

282

557

399

677

ä

Gaps

-756-1.rni

-09 - 733

```
42;
                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447
                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccacgccggccacgagtactactacatctccacgcccactcacaacct
                                                                                                                                                                                                                                                                                                                                 Score 139.6; DB 5;
Pred. No. 4.8e-20;
); Mismatches 134;
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11869
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-011CPPC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TYPE: Floppy disk
SR: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATATCTACTGCCCACACTA---
                                                                                                                                                                                                                                                                                                                                 8.0%;
ilarity 62.4%;
Conservative
                                                                                                                                                                                                                                                                                     sig_peptide
255..324
                                                                                                                                                                                                                                                        3'UTR
892..1809
                                                                                                                                                                                                    CDS
265..891
                                                                                                                                                                                    CDNA
                                                                                                                                                                                                                              5'UTR
1..264
                   OPERATING SYSTEM:
                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 292; Conser
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
  MEDIUM TYP COMPUTER:
                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                    : NAME/KEY:
; LOCATION:
PCT-US95-11869-1
                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                         TOPOLOGY
                                                                                                                                                                                                                                NAME/KEY
                                                                                                                                                                                                                                                           NAME/KEY
                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 678
                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                              qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Óζ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
```

3;

Gaps

338

9

398

162

458

497

399

677

617

```
----ggggcgccgctgccggccgagcgcatggagcact
                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                           Score 135.4; DB 1;
Pred. No. 2.2e-19;
); Mismatches 66;
RESULT 15
US-09-609-324A-7
Sequence 7, Application US/09609324A
; Patent No. RE37582
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: CYTOKINE DESIGNATED LERK-6
; FILE REFERENCE: A7772
CURRENT APPLICATION NUMBER: US/09/609,324A
; CURRENT FILING DATE: 2000-06-30
; PRIOR FILING DATE: 1997-08-29
; PRIOR FILING DATE: 1997-08-39
; PRIOR FILING DATE: 1995-10-03
; PRIOR FILING DATE: 1995-10-03
; PRIOR FILING DATE: 1994-10-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09:49:40
                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.9%;
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13,
                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (2)..(313)
S-09-609-324A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               July
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actacatct
                                                                                                                                                                                                             TYPE: DNA ORGANISM: LERK-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actacatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed:
Job time: 4015 sec
                                                                                                                                                                                                                                                                                                                                                                                                    at----
                                                                                                                                                                                                  LENGTH: 314
                                                                                                                                                                                        SEQ ID NO 7
                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                       123
                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                    αq
                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                         ð
```

2

359

245